

101	258	8.2	1523	2	US-10-012-231A-198	Sequence 198, Appl	174	211	6.7	513	2	US-10-015-393A-385	Sequence 385, App
102	258	8.2	1523	2	US-10-015-389A-198	Sequence 198, Appl	175	211	6.7	513	2	US-10-011-833A-385	Sequence 385, App
103	258	8.2	1523	2	US-10-006-768A-198	Sequence 198, Appl	176	211	6.7	513	2	US-10-006-041A-385	Sequence 385, App
104	258	8.2	1523	2	US-10-015-671A-198	Sequence 198, Appl	177	211	6.7	513	2	US-10-012-064A-385	Sequence 385, App
105	258	8.2	1523	2	US-10-015-393A-198	Sequence 198, Appl	178	210.5	6.7	4302	2	US-08-658-136-5	Sequence 5, Appli
106	258	8.2	1523	2	US-10-011-833A-198	Sequence 198, Appl	179	210.5	6.7	4302	2	US-09-052-469-8	Sequence 8, Appli
107	258	8.2	1523	2	US-10-006-041A-198	Sequence 198, Appl	180	210.5	6.7	4302	2	US-08-422-582-8	Sequence 8, Appli
108	258	8.2	1523	2	US-10-012-064A-198	Sequence 198, Appl	181	210.5	6.7	4302	2	US-08-052-262-8	Sequence 8, Appli
109	255.5	8.1	1480	2	US-09-191-647-7	Sequence 7, Appli	182	209	6.7	353	2	US-10-012-231A-397	Sequence 397, App
110	255.5	8.1	1480	2	US-09-540-245A-7	Sequence 7, Appli	183	209	6.7	353	2	US-10-015-389A-397	Sequence 397, App
111	255.5	8.1	1480	2	US-09-540-153-7	Sequence 7, Appli	184	209	6.7	353	2	US-10-006-768A-397	Sequence 397, App
112	255.5	8.1	1480	2	US-09-182-024A-5	Sequence 5, Appli	185	209	6.7	353	2	US-10-015-671A-397	Sequence 397, App
113	255.5	8.1	1480	2	US-10-289-776-7	Sequence 7, Appli	186	209	6.7	353	2	US-10-015-393A-397	Sequence 397, App
114	255.5	8.1	1480	4	PCT-US91-09055-2	Sequence 2, Appli	187	209	6.7	353	2	US-10-011-833A-397	Sequence 397, App
115	253	8.1	567	2	US-10-037-417-106	Sequence 106, App	188	209	6.7	353	2	US-10-006-041A-397	Sequence 397, App
116	252	8.0	566	2	US-09-775-803-12	Sequence 12, Appl	189	209	6.7	353	2	US-10-012-064A-397	Sequence 397, App
117	252	8.0	567	2	US-10-037-417-105	Sequence 105, App	190	209	6.7	1091	2	US-08-986-485-5	Sequence 5, Appli
118	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appl	191	208.5	6.7	424	2	US-09-949-016-7950	Sequence 7950, Ap
119	249.5	8.0	789	2	US-09-831-846-2	Sequence 2, Appli	192	207.5	6.6	415	2	US-09-935-430-659	Sequence 659, App
120	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appli	193	207.5	6.6	440	2	US-08-964-956-29	Sequence 29, Appl
121	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, Ap	194	207.5	6.6	798	2	US-09-935-430-658	Sequence 658, App
122	247.5	7.9	1525	2	US-09-191-647-2	Sequence 2, Appli	195	207.5	6.6	798	2	US-09-964-956-28	Sequence 28, Appl
123	247.5	7.9	1525	2	US-09-540-245A-2	Sequence 2, Appli	196	206.5	6.6	1101	2	US-08-986-485-2	Sequence 2, Appli
124	247.5	7.9	1525	2	US-09-540-153-2	Sequence 2, Appli	197	206	6.6	428	2	US-09-949-016-6625	Sequence 6625, Ap
125	247.5	7.9	1525	2	US-10-289-776-2	Sequence 2, Appli	198	206	6.6	433	2	US-09-949-016-8521	Sequence 8521, Ap
126	247.5	7.9	1529	2	US-10-188-485-67	Sequence 67, Appl	199	205	6.5	4339	2	US-08-052-469-6	Sequence 6, Appli
127	246.5	7.9	1529	2	US-09-312-283C-396	Sequence 396, App	200	205	6.5	4339	2	US-08-422-582-6	Sequence 6, Appli
128	244	7.8	708	2	US-09-131-648-2	Sequence 2, Appli	201	205	6.5	4339	2	US-08-052-262-6	Sequence 6, Appli
129	244	7.8	708	2	US-09-907-794A-69	Sequence 69, Appl	202	203.5	6.5	4303	1	US-08-460-751-2	Sequence 2, Appli
130	244	7.8	708	2	US-09-905-125A-69	Sequence 69, Appl	203	203.5	6.5	4303	2	US-09-479-467A-2	Sequence 2, Appli
131	244	7.8	708	2	US-09-902-775A-69	Sequence 69, Appl	204	203.5	6.5	4303	2	US-09-655-160-2	Sequence 2, Appli
132	244	7.8	708	2	US-09-906-700-69	Sequence 69, Appl	205	200.5	6.4	302	2	US-09-482-273-105	Sequence 105, App
133	244	7.8	708	2	US-09-903-603A-69	Sequence 69, Appl	206	200.5	6.4	724	2	US-10-104-047-2224	Sequence 2224, Ap
134	244	7.8	708	2	US-09-904-920A-69	Sequence 69, Appl	207	199	6.3	321	2	US-10-104-047-2504	Sequence 2504, Ap
135	244	7.8	708	2	US-09-909-064-69	Sequence 69, Appl	208	198.5	6.3	1338	2	US-09-631-603-2	Sequence 24, Appl
136	244	7.8	708	2	US-09-905-381A-69	Sequence 69, Appl	209	197.5	6.3	616	2	US-10-012-231A-24	Sequence 24, Appl
137	244	7.8	708	2	US-09-906-618-69	Sequence 69, Appl	210	197.5	6.3	616	2	US-10-015-389A-24	Sequence 24, Appl
138	244	7.8	708	2	US-09-906-646-69	Sequence 69, Appl	211	197.5	6.3	616	2	US-10-006-768A-24	Sequence 24, Appl
139	244	7.8	708	2	US-09-904-462-69	Sequence 69, Appl	212	197.5	6.3	616	2	US-10-015-671A-24	Sequence 24, Appl
140	244	7.8	708	2	US-09-902-736A-69	Sequence 69, Appl	213	197.5	6.3	616	2	US-10-015-393A-24	Sequence 24, Appl
141	244	7.8	708	2	US-09-906-722A-69	Sequence 69, Appl	214	197.5	6.3	616	2	US-10-011-833A-24	Sequence 24, Appl
142	243.5	7.8	312	2	US-10-037-417-108	Sequence 108, App	215	197.5	6.3	616	2	US-10-006-041A-24	Sequence 24, Appl
143	241	7.7	380	2	US-09-461-325-161	Sequence 161, App	216	197.5	6.3	616	2	US-10-012-064A-24	Sequence 24, Appl
144	241	7.7	380	2	US-10-012-542-161	Sequence 161, App	217	196.5	6.3	716	2	US-08-312-283C-183	Sequence 183, App
145	241	7.7	380	2	US-10-115-123-161	Sequence 161, App	218	196.5	6.3	771	2	US-09-188-930-183	Sequence 183, App
146	240	7.7	560	2	US-08-592-500-2	Sequence 2, Appli	219	195.5	6.2	553	2	US-10-037-417-28	Sequence 28, Appl
147	240	7.7	560	2	US-08-195-006-2	Sequence 2, Appli	220	195	6.2	620	2	US-09-907-794A-73	Sequence 73, Appl
148	240	7.7	560	2	US-09-063-950-4	Sequence 4, Appli	221	195	6.2	620	2	US-09-905-125A-73	Sequence 73, Appl
149	240	7.7	560	2	US-09-775-803-14	Sequence 14, Appl	222	195	6.2	620	2	US-09-902-775A-73	Sequence 73, Appl
150	240	7.7	560	4	PCT-US94-07644A-2	Sequence 2, Appli	223	195	6.2	620	2	US-09-906-700-73	Sequence 73, Appl
151	236.5	7.5	222	4	PCT-US91-09055-3	Sequence 3, Appli	224	195	6.2	620	2	US-09-903-603A-73	Sequence 73, Appl
152	236.5	7.5	231	152	US-08-986-485-7	Sequence 7, Appli	225	195	6.2	620	2	US-09-904-920A-73	Sequence 73, Appl
153	227	7.2	568	2	US-09-673-245-14	Sequence 14, Appl	226	195	6.2	620	2	US-09-909-064-73	Sequence 73, Appl
154	226.5	7.2	557	2	US-10-037-417-95	Sequence 95, Appl	227	195	6.2	620	2	US-09-905-381A-73	Sequence 73, Appl
155	225	7.2	735	2	US-09-191-647-9	Sequence 9, Appli	228	195	6.2	620	2	US-09-906-618-73	Sequence 73, Appl
156	225	7.2	735	2	US-09-540-245A-9	Sequence 9, Appli	229	195	6.2	620	2	US-09-906-646-73	Sequence 73, Appl
157	225	7.2	735	2	US-09-540-153-9	Sequence 9, Appli	230	195	6.2	620	2	US-09-904-462-73	Sequence 73, Appl
158	225	7.2	735	2	US-10-289-776-9	Sequence 9, Appli	231	195	6.2	620	2	US-09-902-736A-73	Sequence 73, Appl
159	222.5	7.1	536	2	US-09-538-092-992	Sequence 992, App	232	195	6.2	620	2	US-09-906-722A-73	Sequence 73, Appl
160	222	7.1	196	4	PCT-US91-09055-5	Sequence 5, Appli	233	195	6.2	742	2	US-10-104-047-2807	Sequence 2807, Ap
161	222	7.1	498	2	US-10-188-495-51	Sequence 51, Appl	234	195	6.2	832	2	US-09-935-430-660	Sequence 660, App
162	222	7.1	591	2	US-10-188-495-50	Sequence 50, Appl	235	195	6.2	853	2	US-09-964-956-30	Sequence 30, Appl
163	221.5	7.1	557	2	US-10-037-417-94	Sequence 94, Appl	236	194.5	6.2	699	2	US-09-949-016-6073	Sequence 6073, Ap
164	220.5	7.0	841	2	US-09-935-430-657	Sequence 657, App	237	194.5	6.2	720	2	US-09-949-016-9819	Sequence 9819, Ap
165	220.5	7.0	841	2	US-09-964-956-2	Sequence 2, Appli	238	193.5	6.2	224	4	PCT-US91-09055-4	Sequence 4, Appli
166	218.5	7.0	359	2	US-09-949-016-9732	Sequence 9732, Ap	239	193.5	6.2	542	2	US-10-037-417-97	Sequence 97, Appl
167	217.5	6.9	562	2	US-09-673-245-7	Sequence 7, Appli	240	190	6.1	1059	2	US-09-907-794A-290	Sequence 290, App
168	217.5	6.9	837	2	US-09-964-956-5	Sequence 5, Appli	241	190	6.1	1059	2	US-09-905-125A-290	Sequence 290, App
169	214.5	6.8	255	2	US-09-893-737-232	Sequence 232, App	242	190	6.1	1059	2	US-09-902-775A-290	Sequence 290, App
170	211	6.7	513	2	US-10-012-231A-385	Sequence 385, App	243	190	6.1	1059	2	US-09-906-700-290	Sequence 290, App
171	211	6.7	513	2	US-10-015-389A-385	Sequence 385, App	244	190	6.1	1059	2	US-09-903-603A-290	Sequence 290, App
172	211	6.7	513	2	US-10-006-768A-385	Sequence 385, App	245	190	6.1	1059	2	US-09-904-920A-290	Sequence 290, App
173	211	6.7	513	2	US-10-015-671A-385	Sequence 385, App	246	190	6.1	1059	2	US-09-909-064-290	Sequence 290, App

247	190	6.1	1059	2	US-09-905-381A-290	Sequence 290, App	320	167	5.3	746	4	PCT-US95-10509-2	Sequence 2, Appli
248	190	6.1	1059	2	US-09-906-618-290	Sequence 290, App	321	167	5.3	1112	2	US-09-353-585-3	Sequence 3, Appli
249	190	6.1	1059	2	US-09-906-646-290	Sequence 290, App	322	166.5	5.3	224	2	US-09-482-273-174	Sequence 174, App
250	190	6.1	1059	2	US-09-904-463-290	Sequence 290, App	323	166	5.3	1112	2	US-09-353-585-2	Sequence 2, Appli
251	190	6.1	1059	2	US-09-903-736A-290	Sequence 290, App	324	164.5	5.2	501	2	US-09-907-794A-185	Sequence 185, App
252	190	6.1	1059	2	US-09-906-722A-290	Sequence 290, App	325	164.5	5.2	501	2	US-09-905-125A-185	Sequence 185, App
253	190	6.1	1119	2	US-09-907-794A-294	Sequence 294, App	326	164.5	5.2	501	2	US-09-902-775A-185	Sequence 185, App
254	190	6.1	1119	2	US-09-905-125A-294	Sequence 294, App	327	164.5	5.2	501	2	US-09-906-700-185	Sequence 185, App
255	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App	328	164.5	5.2	501	2	US-09-903-603A-185	Sequence 185, App
256	190	6.1	1119	2	US-09-906-700-294	Sequence 294, App	329	164.5	5.2	501	2	US-09-904-920A-185	Sequence 185, App
257	190	6.1	1119	2	US-09-903-603A-294	Sequence 294, App	330	164.5	5.2	501	2	US-09-909-664-185	Sequence 185, App
258	190	6.1	1119	2	US-09-904-920A-294	Sequence 294, App	331	164.5	5.2	501	2	US-09-905-381A-185	Sequence 185, App
259	190	6.1	1119	2	US-09-909-064-294	Sequence 294, App	332	164.5	5.2	501	2	US-09-906-618-185	Sequence 185, App
260	190	6.1	1119	2	US-09-905-381A-294	Sequence 294, App	333	164.5	5.2	501	2	US-09-906-646-185	Sequence 185, App
261	190	6.1	1119	2	US-09-906-618-294	Sequence 294, App	334	164.5	5.2	501	2	US-09-904-462-185	Sequence 185, App
262	190	6.1	1119	2	US-09-906-646-294	Sequence 294, App	335	164.5	5.2	501	2	US-09-902-736A-185	Sequence 185, App
263	190	6.1	1119	2	US-09-904-462-294	Sequence 294, App	336	164.5	5.2	501	2	US-09-906-722A-185	Sequence 185, App
264	190	6.1	1119	2	US-09-902-736A-294	Sequence 294, App	337	164.5	5.2	582	2	US-09-081-149-8	Sequence 8, Appli
265	190	6.1	1119	2	PCT-US91-09055-6	Sequence 6, Appli	338	164.5	5.2	584	2	US-09-949-016-10752	Sequence 10752, A
266	186.5	5.9	196	4	US-09-949-016-9438	Sequence 949, App	339	164.5	5.2	858	2	US-10-104-047-2918	Sequence 2918, Ap
267	186.5	5.9	844	2	US-09-538-092-999	Sequence 938, Ap	340	164	5.2	696	2	US-09-907-794A-91	Sequence 91, Appl
268	186	5.9	440	2	US-09-949-016-9282	Sequence 949, App	341	164	5.2	696	2	US-09-905-125A-91	Sequence 91, Appl
269	186	5.9	451	2	US-07-613-083B-1	Sequence 9282, Ap	342	164	5.2	696	2	US-09-902-775A-91	Sequence 91, Appl
270	184	5.9	320	1	US-09-949-016-6115	Sequence 1, Appli	343	164	5.2	696	2	US-09-906-700-91	Sequence 91, Appl
271	184	5.9	368	2	US-09-949-016-6115	Sequence 6115, Ap	344	164	5.2	696	2	US-09-903-603A-91	Sequence 91, Appl
272	184	5.9	368	2	US-09-715-8336A-9	Sequence 9, Appli	345	164	5.2	696	2	US-09-904-920A-91	Sequence 91, Appl
273	184	5.9	382	2	US-09-949-016-10542	Sequence 10542, A	346	164	5.2	696	2	US-09-909-064-91	Sequence 91, Appl
274	183	5.8	662	2	US-09-538-092-1325	Sequence 1325, Ap	347	164	5.2	696	2	US-09-905-381A-91	Sequence 91, Appl
275	183	5.8	662	2	US-09-949-016-6619	Sequence 6619, Ap	348	164	5.2	696	2	US-09-906-618-91	Sequence 91, Appl
276	183	5.8	665	2	US-09-866-028-2	Sequence 10710, A	349	164	5.2	696	2	US-09-906-646-91	Sequence 91, Appl
277	182.5	5.8	379	2	US-09-944-457-2	Sequence 2, Appli	350	164	5.2	696	2	US-09-904-462-91	Sequence 91, Appl
278	182.5	5.8	379	2	US-09-944-457-2	Sequence 2, Appli	351	164	5.2	696	2	US-09-902-736A-91	Sequence 91, Appl
279	182.5	5.8	379	2	US-09-945-584-2	Sequence 2, Appli	352	164	5.2	696	2	US-09-906-722A-91	Sequence 91, Appl
280	182.5	5.8	379	2	US-09-944-944-2	Sequence 2, Appli	353	164	5.2	904	2	US-09-949-002-352	Sequence 352, App
281	182.5	5.8	379	2	US-09-945-587-2	Sequence 2, Appli	354	164	5.2	910	2	US-09-949-002-483	Sequence 483, App
282	182.5	5.8	958	2	US-09-706-594-5	Sequence 5, Appli	355	163	5.2	582	2	US-09-081-149-7	Sequence 7, Appli
283	182.5	5.8	966	2	US-09-964-956-32	Sequence 32, Appl	356	163	5.2	753	2	US-09-056-383-13	Sequence 13, Appl
284	182	5.8	378	2	US-09-689-486-62	Sequence 62, Appl	357	161	5.1	559	2	US-09-081-149-2	Sequence 2, Appli
285	180	5.7	493	2	US-10-037-417-30	Sequence 30, Appl	358	160	5.1	942	2	US-10-101-464A-911	Sequence 911, App
286	180	5.7	989	2	US-09-954-987B-171	Sequence 171, App	359	158.5	5.1	1032	2	US-09-954-987B-192	Sequence 192, App
287	178	5.7	368	1	US-08-303-238-3	Sequence 3, Appli	360	158	5.0	257	2	US-09-270-767-41554	Sequence 41554, A
288	178	5.7	368	1	US-08-458-834-3	Sequence 3, Appli	361	158	5.0	352	2	US-09-949-016-6781	Sequence 6781, Ap
289	178	5.7	522	2	US-09-991-181-278	Sequence 278, App	362	158	5.0	374	2	US-09-949-016-7689	Sequence 7689, Ap
290	178	5.7	522	2	US-09-990-444-278	Sequence 278, App	363	157.5	5.0	236	1	US-08-442-063A-42	Sequence 42, Appl
291	178	5.7	522	2	US-09-997-333-278	Sequence 278, App	364	157.5	5.0	672	2	US-09-949-002-522	Sequence 522, App
292	178	5.7	522	2	US-09-992-598-278	Sequence 278, App	365	157.5	5.0	796	2	US-10-104-047-2293	Sequence 2293, Ap
293	178	5.7	1049	2	US-09-999-833A-496	Sequence 496, App	366	156.5	5.0	376	2	US-09-538-092-1276	Sequence 1276, Ap
294	178	5.7	1049	2	US-09-954-987B-170	Sequence 170, App	367	156	5.0	975	2	US-09-949-016-7595	Sequence 7595, Ap
295	178	5.7	1049	2	US-10-020-445A-496	Sequence 496, App	368	155	4.9	1041	2	US-09-999-833A-498	Sequence 498, App
296	178	5.7	1052	2	US-09-949-016-11508	Sequence 11508, A	369	155	4.9	1041	2	US-09-954-987B-184	Sequence 184, App
297	177.5	5.7	1050	2	US-09-954-987B-175	Sequence 175, App	370	155	4.9	1041	2	US-09-954-987B-186	Sequence 186, App
298	176.5	5.6	522	2	US-10-104-047-2664	Sequence 2664, Ap	371	155	4.9	1041	2	US-10-020-445A-498	Sequence 498, App
299	175	5.6	368	6	5340934-2	Patent No. 5340934	372	155	4.9	1059	2	US-09-954-987B-187	Sequence 187, App
300	173.5	5.5	998	2	US-10-101-464A-914	Sequence 914, App	373	154.5	4.9	377	2	US-09-949-016-7949	Sequence 7949, Ap
301	172.5	5.5	287	1	US-08-442-063A-45	Sequence 45, Appl	374	154.5	4.9	1495	2	US-08-522-726B-1	Sequence 1, Appli
302	172.5	5.5	307	1	US-08-442-063A-48	Sequence 48, Appl	375	154.5	4.9	894	1	US-08-372-892-1	Sequence 2, Appli
303	172.5	5.5	333	1	US-08-442-063A-27	Sequence 27, Appl	376	153.5	4.9	894	1	US-08-372-892-2	Sequence 34, Appl
304	172.5	5.5	338	1	US-08-689-486-53	Sequence 63, Appl	377	153.5	4.9	894	1	US-08-445-640-34	Sequence 34, Appl
305	172.5	5.5	342	1	US-08-272-319-2	Sequence 2, Appli	378	153.5	4.9	894	1	US-08-170-558-34	Sequence 34, Appl
306	172.5	5.5	342	1	US-08-619-916-2	Sequence 2, Appli	379	153.5	4.9	894	2	US-08-447-314-34	Sequence 34, Appl
307	172.5	5.5	342	1	PCT-US95-08542-2	Sequence 2, Appli	380	153.5	4.9	894	2	US-08-445-461-34	Sequence 34, Appl
308	172.5	5.5	359	1	US-08-303-238-4	Sequence 4, Appli	381	153.5	4.9	894	2	US-09-223-490-34	Sequence 34, Appl
309	172.5	5.5	359	1	US-08-458-834-4	Sequence 4, Appli	382	153.5	4.9	1032	2	US-09-954-987B-6	Sequence 6, Appli
310	172.5	5.5	359	2	US-09-538-092-868	Sequence 868, App	383	153	4.9	679	2	US-09-252-991A-18857	Sequence 18857, A
311	172.5	5.5	359	2	US-09-949-016-6143	Sequence 6143, Ap	384	153	4.9	699	2	US-10-237-551-143	Sequence 143, App
312	172.5	5.5	360	2	US-09-949-016-7925	Sequence 7925, Ap	385	153	4.9	699	2	US-10-237-551-254	Sequence 254, App
313	172.5	5.5	1388	2	US-10-153-469A-10	Sequence 10, Appl	386	153	4.9	1248	2	US-10-042-810-2	Sequence 2, Appli
314	172.5	5.5	1388	2	US-10-154-889-10	Sequence 10, Appl	387	153	4.9	1278	2	US-10-042-810-4	Sequence 4, Appli
315	170.5	5.4	373	2	US-09-724-864-43	Sequence 43, Appl	388	152.5	4.9	364	2	US-10-104-047-2127	Sequence 2127, Ap
316	170	5.4	907	2	US-09-170-496D-264	Sequence 264, App	389	152	4.8	786	2	US-09-949-002-351	Sequence 351, App
317	170	5.4	907	2	US-09-170-496D-278	Sequence 278, App	390	152	4.8	786	2	US-09-949-002-386	Sequence 386, App
318	169.5	5.4	353	6	5340934-4	Patent No. 5340934	391	152	4.8	802	2	US-09-949-002-512	Sequence 512, App
319	168	5.4	1049	2	US-09-954-987B-172	Sequence 172, App	392	151.5	4.8	455	2	US-10-188-495-3	Sequence 3, Appli

393	151.5	4.8	1964	2	US-09-467-997-1	Sequence 1, Appli	466	138.5	4.4	811	2	US-09-997-333-57	Sequence 57, Appli
394	151	4.8	532	2	US-09-270-767-46234	Sequence 46234, A	467	138.5	4.4	811	2	US-09-992-598-57	Sequence 57, Appli
395	150.5	4.8	695	1	US-08-487-886-2	Sequence 2, Appli	468	138	4.4	323	2	US-09-949-016-7924	Sequence 7924, Ap
396	150.5	4.8	695	2	US-08-482-855-2	Sequence 2, Appli	469	137.5	4.4	141	2	US-09-270-767-45511	Sequence 4551, A
397	150.5	4.8	695	2	US-08-474-986-2	GENERAL INFORMA	470	137.5	4.4	884	6	5208144-8	Patent No. 5208144
398	150	4.8	259	2	US-09-907-994A-71	Sequence 71, Appl	471	137	4.4	4544	1	US-08-469-486-52	Sequence 52, Appl
399	150	4.8	259	2	US-09-905-125A-71	Sequence 71, Appl	472	137	4.4	4544	1	US-08-469-658-52	Sequence 52, Appl
400	150	4.8	259	2	US-09-902-775A-71	Sequence 71, Appl	473	136.5	4.4	984	2	US-10-101-464A-919	Sequence 919, App
401	150	4.8	259	2	US-09-906-700-71	Sequence 71, Appl	474	136.5	4.4	2972	2	US-09-579-181-2	Sequence 2, Appli
402	150	4.8	259	2	US-09-903-603A-71	Sequence 71, Appl	475	136.5	4.4	3118	2	US-09-579-181-1	Sequence 1, Appli
403	150	4.8	259	2	US-09-904-920A-71	Sequence 71, Appl	476	136	4.3	287	2	US-10-104-047-3292	Sequence 3292, Ap
404	150	4.8	259	2	US-09-909-064-71	Sequence 71, Appl	477	136	4.3	692	2	US-07-757-342D-6	Sequence 6, Appli
405	150	4.8	259	2	US-09-905-381A-71	Sequence 71, Appl	478	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appli
406	150	4.8	259	2	US-09-906-618-71	Sequence 71, Appl	479	135.5	4.3	536	2	US-09-252-991A-31124	Sequence 31124, A
407	150	4.8	259	2	US-09-906-646-71	Sequence 71, Appl	480	135.5	4.3	743	2	US-09-771-161A-164	Sequence 164, App
408	150	4.8	259	2	US-09-904-462-71	Sequence 71, Appl	481	135.5	4.3	743	2	US-09-771-161A-254	Sequence 254, App
409	150	4.8	259	2	US-09-902-736A-71	Sequence 71, Appl	482	135	4.3	446	2	US-10-101-464A-733	Sequence 733, App
410	150	4.8	259	2	US-09-906-722A-71	Sequence 71, Appl	483	135	4.3	538	2	US-09-616-289-43	Sequence 43, Appl
411	150	4.8	513	2	US-09-068-804-14	Sequence 14, Appl	484	135	4.3	538	2	US-09-976-740-43	Sequence 43, Appli
412	149	4.8	503	2	US-10-037-417-104	Sequence 104, App	485	135	4.3	723	2	US-09-434-408-2	Sequence 2, Appli
413	149	4.8	1012	1	US-08-475-891A-4	Sequence 4, Appli	486	135	4.3	723	2	US-10-104-047-2572	Sequence 2572, Ap
414	149	4.8	1025	1	US-08-567-375-4	Sequence 4, Appli	487	135	4.3	907	2	US-08-783-774-2	Sequence 2, Appli
415	149	4.8	1025	1	US-08-587-680A-4	Sequence 4, Appli	488	135	4.3	907	2	US-09-328-599A-1	Sequence 1, Appli
416	149	4.8	1026	2	US-09-623-551-18	Sequence 18, Appl	489	135	4.3	907	4	PCT-US95-04611A-19	Sequence 19, Appl
417	149	4.8	1504	2	US-09-364-206-2	Sequence 2, Appli	490	134.5	4.3	802	2	US-09-823-240A-2	Sequence 2, Appli
418	149	4.8	1874	2	US-09-331-403-2	Sequence 2, Appli	491	134	4.3	536	2	US-09-232-225-21	Sequence 21, Appl
419	148.5	4.7	375	1	US-08-458-838-2	Sequence 2, Appli	492	134	4.3	550	2	US-09-616-289-47	Sequence 47, Appl
420	148.5	4.7	375	2	US-08-458-838-2	Sequence 2, Appli	493	134	4.3	550	2	US-09-976-740-47	Sequence 47, Appl
421	147.5	4.7	570	2	US-09-565-501A-104	Sequence 104, App	494	134	4.3	555	2	US-09-232-225-15	Sequence 15, Appl
422	147.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App	495	134	4.3	555	2	US-09-292-225-18	Sequence 18, Appl
423	147.5	4.7	570	2	US-09-874-923-104	Sequence 104, App	496	133.5	4.3	1166	2	US-10-101-464A-900	Sequence 900, App
424	147.5	4.7	1728	2	US-09-943-002-532	Sequence 532, App	497	133	4.2	652	2	US-10-104-047-3364	Sequence 3364, Ap
425	147	4.7	177	2	US-09-270-767-32705	Sequence 32705, A	498	133	4.2	4391	2	US-10-086-011A-2	Sequence 2, Appli
426	147	4.7	177	2	US-09-270-767-47922	Sequence 47922, A	499	132.5	4.2	390	2	US-08-460-576-2	Sequence 2, Appli
427	147	4.7	265	2	US-09-270-767-45056	Sequence 45056, A	500	132.5	4.2	463	1	US-08-162-402B-9	Sequence 9, Appli
428	147	4.7	2414	1	US-08-227-536-2	Sequence 2, Appli	501	132.5	4.2	579	2	US-09-325-932A-185	Sequence 185, App
429	147	4.7	2414	2	US-09-538-092-1289	Sequence 1289, Ap	502	132.5	4.2	583	2	US-09-641-612-2	Sequence 2, Appli
430	147	4.7	2414	4	PCT-US95-04682-2	Sequence 2, Appli	503	132.5	4.2	2035	1	US-08-046-585-5	Sequence 5, Appli
431	146.5	4.7	325	2	US-10-104-047-3320	Sequence 3320, Ap	504	132.5	4.2	2035	4	PCT-US93-11721-5	Sequence 5, Appli
432	146.5	4.7	344	2	US-10-104-047-3358	Sequence 3358, Ap	505	132.5	4.2	2035	1	US-08-393-703-5	Sequence 5, Appli
433	146.5	4.7	1404	1	US-08-400-159-2	Sequence 2, Appli	506	132.5	4.2	2045	2	US-09-949-016-10491	Sequence 201, App
434	146.5	4.7	1404	2	US-08-611-729A-2	Sequence 2, Appli	507	132.5	4.2	3122	2	US-10-237-551-201	Sequence 201, App
435	146.5	4.7	1404	2	US-09-195-524-2	Sequence 2, Appli	508	132.5	4.2	3122	2	US-10-237-551-250	Sequence 250, App
436	146	4.7	786	2	US-09-103-429A-3	Sequence 3, Appli	509	132	4.2	287	2	US-09-893-737-110	Sequence 110, App
437	146	4.7	788	2	US-09-294-663-3	Sequence 3, Appli	510	132	4.2	465	1	US-08-162-402B-8	Sequence 8, Appli
438	146	4.7	885	1	US-08-372-892-4	Sequence 4, Appli	511	132	4.2	705	2	US-10-101-464A-894	Sequence 894, App
439	146	4.7	885	2	US-09-919-497-52	Sequence 52, Appl	512	132	4.2	979	2	US-08-514-213A-2	Sequence 2, Appli
440	145.5	4.6	2142	2	US-09-538-092-1142	Sequence 1142, Ap	513	132	4.2	979	2	US-09-015-399-5	Sequence 5, Appli
441	145.5	4.6	2142	2	US-09-949-002-371	Sequence 371, App	514	132	4.2	1003	2	US-09-949-016-11260	Sequence 11260, A
442	145	4.6	353	2	US-09-949-016-7923	Sequence 7923, Ap	515	131.5	4.2	461	2	US-10-037-417-96	Sequence 96, Appl
443	145	4.6	1032	2	US-09-954-987B-3	Sequence 3, Appli	516	131.5	4.2	571	2	US-09-252-991A-30533	Sequence 30533, A
444	144	4.6	661	1	US-08-514-014-4	Sequence 4, Appli	517	131	4.2	180	2	US-08-986-485-8	Sequence 8, Appli
445	144	4.6	661	1	US-08-833-823-4	Sequence 4, Appli	518	131	4.2	227	2	US-10-101-464A-666	Sequence 666, App
446	143.5	4.6	1274	1	US-09-095-443-2	Sequence 2, Appli	519	131	4.2	279	2	US-09-270-767-41558	Sequence 41558, A
447	143	4.6	935	2	US-09-477-962-107	Sequence 107, App	520	131	4.2	407	2	US-09-270-767-46649	Sequence 46649, A
448	142.5	4.5	141	2	US-09-270-767-31706	Sequence 31706, A	521	131	4.2	799	2	US-09-180-439-6	Sequence 6, Appli
449	142.5	4.5	141	2	US-09-270-767-46923	Sequence 46923, A	522	131	4.2	947	2	US-09-228-986-73	Sequence 73, Appl
450	142.5	4.5	807	2	US-09-103-429A-4	Sequence 4, Appli	523	131	4.2	947	2	US-10-101-464A-73	Sequence 73, Appl
451	142.5	4.5	807	2	US-09-294-663-4	Sequence 4, Appli	524	131	4.2	1062	2	US-09-902-540-16313	Sequence 16313, A
452	142	4.5	326	2	US-09-689-486-64	Sequence 64, Appl	525	131	4.2	1196	2	US-08-881-706-2	Sequence 2, Appli
453	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appli	526	131	4.2	1196	2	US-09-823-394-2	Sequence 2, Appli
454	142	4.5	365	2	US-10-101-464A-901	Sequence 901, App	527	131	4.2	1938	2	US-09-949-016-6609	Sequence 6609, Ap
455	142	4.5	435	2	US-10-188-495-5	Sequence 5, Appli	528	130.5	4.2	843	2	US-10-101-464A-893	Sequence 893, App
456	142	4.5	661	2	US-10-037-417-107	Sequence 107, App	529	130.5	4.2	878	2	US-09-556-706B-2	Sequence 2, Appli
457	140.5	4.5	345	2	US-10-101-464A-802	Sequence 802, App	530	130.5	4.2	878	2	US-09-724-418A-2	Sequence 4, Appli
458	140.5	4.5	376	1	US-08-303-238-1	Sequence 1, Appli	531	130.5	4.2	3729	1	US-08-804-227C-4	Sequence 4, Appli
459	140.5	4.5	376	2	US-08-458-834-1	Sequence 1, Appli	532	130	4.1	619	2	US-10-037-417-34	Sequence 34, Appl
460	140	4.5	283	2	US-09-949-016-7910	Sequence 7910, Ap	533	130	4.1	645	2	US-10-101-464A-920	Sequence 920, App
461	140	4.5	547	2	US-10-101-464A-928	Sequence 928, App	534	129.5	4.1	550	2	US-09-252-991A-21295	Sequence 21295, A
462	139	4.4	5179	2	US-09-538-092-1258	Sequence 1258, Ap	535	129.5	4.1	912	4	PCT-US95-03747-2	Sequence 2, Appli
463	138.5	4.4	710	2	US-10-104-047-3402	Sequence 3402, Ap	536	129	4.1	363	2	US-09-270-767-44030	Sequence 44030, A
464	138.5	4.4	811	2	US-09-991-181-57	Sequence 57, Appl	537	129	4.1	823	2	US-09-252-991A-23655	Sequence 23655, A
465	138.5	4.4	811	2	US-09-990-444-57	Sequence 57, Appl	538	129	4.1	885	2	US-09-252-991A-26129	Sequence 26129, A

539	129	4.1	1133	2	US-10-101-464A-809	Sequence 809, App	612	124.5	4.0	546	2	US-09-906-700-250	Sequence 250, App
540	129	4.1	1940	1	US-08-644-271-30	Sequence 30, Appl	613	124.5	4.0	546	2	US-09-903-603A-250	Sequence 250, App
541	129	4.1	1940	2	US-08-077-955-34	Sequence 34, Appl	614	124.5	4.0	546	2	US-09-904-920A-250	Sequence 250, App
542	129	4.1	1940	2	US-10-016-283-34	Sequence 34, Appl	615	124.5	4.0	546	2	US-09-909-064-250	Sequence 250, App
543	129	4.1	2321	2	US-09-230-652-2	Sequence 2, Appl	616	124.5	4.0	546	2	US-09-905-381A-250	Sequence 250, App
544	128.5	4.1	188	1	US-08-442-063A-39	Sequence 39, Appl	617	124.5	4.0	546	2	US-09-906-618-250	Sequence 250, App
545	128.5	4.1	446	1	US-08-836-854-15	Sequence 15, Appl	618	124.5	4.0	546	2	US-09-906-646-250	Sequence 250, App
546	128.5	4.1	508	2	US-10-104-047-3233	Sequence 3233, Ap	619	124.5	4.0	546	2	US-09-904-462-250	Sequence 250, App
547	128.5	4.1	653	2	US-10-101-464A-953	Sequence 953, App	620	124.5	4.0	546	2	US-09-902-722A-250	Sequence 250, App
548	128.5	4.1	864	2	US-10-101-464A-896	Sequence 896, App	621	124.5	4.0	546	2	US-09-906-722A-250	Sequence 250, App
549	128.5	4.1	865	2	US-09-902-540-10416	Sequence 10416, A	622	124.5	4.0	623	2	US-09-949-016-6530	Sequence 6530, Ap
550	128.5	4.1	1023	1	US-08-475-851A-2	Sequence 2, Appl	623	124.5	4.0	998	2	US-10-101-464A-895	Sequence 895, App
551	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appl	624	124.5	4.0	1042	2	US-09-252-991A-30444	Sequence 30444, A
552	128.5	4.1	1023	1	US-08-587-680A-2	Sequence 2, Appl	625	124.5	4.0	1709	2	US-09-949-016-10503	Sequence 10503, A
553	128	4.1	475	2	US-09-252-991A-30242	Sequence 30242, A	626	124	4.0	277	2	US-07-741-453A-58	Sequence 58, Appl
554	128	4.1	538	1	US-08-541-759B-2	Sequence 2, Appl	627	124	4.0	707	2	US-09-228-986-80	Sequence 80, Appl
555	128	4.1	717	2	US-10-101-464A-810	Sequence 810, App	628	124	4.0	707	2	US-10-101-464A-80	Sequence 80, Appl
556	127.5	4.1	1006	2	US-10-415-147-12	Sequence 12, Appl	629	124	4.0	1457	2	US-08-665-259-27	Sequence 27, Appl
557	127.5	4.1	1522	2	US-10-144-198-31	Sequence 31, Appl	630	124	4.0	1457	2	US-08-762-500-27	Sequence 27, Appl
558	127.5	4.1	1581	2	US-09-949-002-414	Sequence 414, App	631	124	4.0	1472	2	US-09-032-438C-119	Sequence 119, App
559	127.5	4.1	3969	2	US-08-061-376-5	Sequence 5, Appl	632	123.5	3.9	1312	2	US-09-041-886-19	Sequence 19, Appl
560	127.5	4.1	3969	2	US-09-538-092-1262	Sequence 1262, Ap	633	123.5	3.9	1312	2	US-09-648-281-2	Sequence 2, Appl
561	127	4.1	260	2	US-09-270-767-32658	Sequence 32658, A	634	123.5	3.9	1312	2	US-09-707-919A-19	Sequence 19, Appl
562	127	4.1	615	2	US-09-252-991A-26695	Sequence 26695, A	635	123.5	3.9	1312	2	US-09-083-268-3	Sequence 3, Appl
563	126.5	4.0	141	2	US-09-270-767-32244	Sequence 32244, A	636	123.5	3.9	1312	2	US-08-981-998A-3	Sequence 3, Appl
564	126.5	4.0	438	2	US-09-270-767-47461	Sequence 47461, A	637	123	3.9	526	2	US-10-101-464A-898	Sequence 898, App
565	126.5	4.0	438	2	US-09-991-181-129	Sequence 129, App	638	123	3.9	557	2	US-09-248-796A-26892	Sequence 26892, A
566	126.5	4.0	438	2	US-09-990-444-129	Sequence 129, App	639	123	3.9	888	1	US-08-445-640-35	Sequence 35, Appl
567	126.5	4.0	438	2	US-09-987-333-129	Sequence 129, App	640	123	3.9	888	2	US-08-170-558-35	Sequence 35, Appl
568	126.5	4.0	438	2	US-09-992-598-129	Sequence 129, App	641	123	3.9	888	2	US-08-447-314-35	Sequence 35, Appl
569	126.5	4.0	659	2	US-09-423-753-3	Sequence 3, Appl	642	123	3.9	888	2	US-08-445-461-35	Sequence 35, Appl
570	126.5	4.0	685	2	US-08-872-855-2	Sequence 2, Appl	643	123	3.9	888	2	US-09-223-490-35	Sequence 35, Appl
571	126.5	4.0	685	2	US-09-423-753-25	Sequence 25, Appl	644	123	3.9	924	1	US-08-481-130-28	Sequence 28, Appl
572	126.5	4.0	685	2	US-09-641-612-7	Sequence 7, Appl	645	123	3.9	924	1	US-08-656-984A-28	Sequence 28, Appl
573	126.5	4.0	919	2	US-10-101-464A-642	Sequence 642, App	646	123	3.9	924	1	US-08-485-604-28	Sequence 28, Appl
574	126.5	4.0	999	1	US-08-473-553A-5	Sequence 5, Appl	647	123	3.9	924	1	US-08-487-595-28	Sequence 28, Appl
575	126	4.0	143	2	US-09-893-737-190	Sequence 190, App	648	123	3.9	924	1	US-09-248-796A-16546	Sequence 16546, A
576	126	4.0	152	2	US-09-270-767-33594	Sequence 33594, A	649	122.5	3.9	494	2	US-09-641-612-5	Sequence 5, Appl
577	126	4.0	775	2	US-09-949-016-8799	Sequence 8799, Ap	650	122.5	3.9	585	2	US-09-252-991A-18875	Sequence 3, Appl
578	126	4.0	1485	2	US-09-762-569-4	Sequence 4, Appl	651	122.5	3.9	585	2	US-09-180-439-3	Sequence 3, Appl
579	126	4.0	1821	2	US-09-949-016-5938	Sequence 5938, Ap	652	122.5	3.9	968	2	US-09-180-439-4	Sequence 4, Appl
580	125.5	4.0	258	2	US-10-012-231A-153	Sequence 153, App	653	122.5	3.9	968	2	US-09-180-439-8	Sequence 8, Appl
581	125.5	4.0	258	2	US-10-015-389A-153	Sequence 153, App	654	122.5	3.9	1016	2	US-09-771-161A-255	Sequence 255, App
582	125.5	4.0	258	2	US-10-006-768A-153	Sequence 153, App	655	122.5	3.9	1036	2	US-09-771-161A-256	Sequence 256, App
583	125.5	4.0	258	2	US-10-015-671A-153	Sequence 153, App	656	122.5	3.9	1036	2	US-09-461-325-186	Sequence 186, App
584	125.5	4.0	258	2	US-10-015-393A-153	Sequence 153, App	657	122	3.9	131	2	US-10-012-542-186	Sequence 186, App
585	125.5	4.0	258	2	US-10-011-833A-153	Sequence 153, App	658	122	3.9	131	2	US-10-115-123-412	Sequence 412, App
586	125.5	4.0	258	2	US-10-006-041A-153	Sequence 153, App	659	122	3.9	191	2	US-10-115-123-412	Sequence 412, App
587	125.5	4.0	258	2	US-10-012-064A-153	Sequence 153, App	660	122	3.9	206	2	US-09-461-325-412	Sequence 412, App
588	125.5	4.0	440	2	US-09-985-335-3	Sequence 3, Appl	661	122	3.9	206	2	US-10-012-542-412	Sequence 412, App
589	125.5	4.0	440	2	US-09-410-372-3	Sequence 3, Appl	662	122	3.9	206	2	US-10-115-123-412	Sequence 412, App
590	125.5	4.0	764	2	US-07-741-453A-54	Sequence 54, Appl	663	122	3.9	312	2	US-09-270-767-31750	Sequence 31750, A
591	125.5	4.0	1129	2	US-07-741-453A-60	Sequence 60, Appl	664	122	3.9	328	1	US-08-414-526A-9	Sequence 9, Appl
592	125.5	4.0	764	2	US-09-023-905A-2	Sequence 2, Appl	665	122	3.9	328	1	US-08-926-922-9	Sequence 9, Appl
593	125	4.0	419	2	US-10-002-344A-237	Sequence 237, App	666	122	3.9	328	2	US-09-253-682-9	Sequence 9, Appl
594	125	4.0	757	2	US-09-252-991A-25918	Sequence 25918, A	667	122	3.9	328	2	US-09-527-657-9	Sequence 9, Appl
595	125	4.0	957	2	US-09-252-991A-20408	Sequence 20408, A	668	122	3.9	328	2	US-09-832-100-9	Sequence 9, Appl
596	125	4.0	1139	2	US-09-513-505-2	Sequence 2, Appl	669	122	3.9	481	2	US-09-949-016-9748	Sequence 9748, Ap
597	125	4.0	2023	2	US-09-491-356C-8	Sequence 8, Appl	670	122	3.9	495	2	US-09-252-991A-31949	Sequence 31949, A
598	125	4.0	2026	2	US-09-487-558B-86	Sequence 86, Appl	671	122	3.9	515	2	US-09-252-991A-28127	Sequence 28127, A
599	125	4.0	2124	2	US-09-538-092-1377	Sequence 1377, Ap	672	122	3.9	527	2	US-09-370-838-216	Sequence 216, App
600	125	4.0	2094	2	US-09-252-991A-17231	Sequence 17231, A	673	122	3.9	527	2	US-09-854-133-216	Sequence 216, App
601	124.5	4.0	124	5	US-09-270-767-61021	Sequence 61021, A	674	122	3.9	529	2	US-09-716-964B-2	Sequence 2, Appl
602	124.5	4.0	298	2	US-09-232-160-17	Sequence 17, Appl	675	121.5	3.9	320	2	US-09-325-932A-190	Sequence 190, App
603	124.5	4.0	298	2	US-09-800-729-87	Sequence 87, Appl	676	121.5	3.9	497	2	US-09-252-991A-19831	Sequence 19831, A
604	124.5	4.0	298	2	US-09-800-729-121	Sequence 121, App	677	121.5	3.9	695	2	US-09-248-796A-18020	Sequence 18020, A
605	124.5	4.0	298	2	US-10-000-489-22	Sequence 22, Appl	678	121.5	3.9	818	2	US-10-104-047-2546	Sequence 2546, Ap
606	124.5	4.0	298	2	US-09-832-129-50	Sequence 50, Appl	679	121.5	3.9	1225	2	US-09-501-171-4	Sequence 4, Appl
607	124.5	4.0	307	2	US-09-949-016-9817	Sequence 9817, Ap	680	121.5	3.9	1225	4	PCT-US95-02251-3	Sequence 6063, Ap
608	124.5	4.0	307	2	US-09-949-016-9818	Sequence 9818, Ap	681	121.5	3.9	1251	3	US-09-949-016-6063	Sequence 3, Appl
609	124.5	4.0	546	2	US-09-907-794A-250	Sequence 250, App	682	121.5	3.9	1252	1	US-08-199-780-3	Sequence 3, Appl
610	124.5	4.0	546	2	US-09-905-125A-250	Sequence 250, App	683	121.5	3.9	1252	1	US-08-316-650-3	Sequence 3, Appl
611	124.5	4.0	546	2	US-09-902-775A-250	Sequence 250, App	684	121.5	3.9	1253	2	US-08-479-722B-4	Sequence 4, Appl

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686	121	3.9	499	2	US-09-049-672A-1	Sequence 1, Appli	759	117.5	3.7	190	2	US-08-776-207-4	Sequence 4, Appli
687	121	3.9	739	2	US-09-902-540-10606	Sequence 10606, A	760	117.5	3.7	190	2	US-09-507-773-4	Sequence 4, Appli
688	121	3.9	910	2	US-09-228-986-72	Sequence 72, Appli	761	117.5	3.7	190	2	US-10-016-447-4	Sequence 4, Appli
689	121	3.9	910	2	US-10-101-464A-72	Sequence 72, Appli	762	117.5	3.7	190	4	PCT-US95-09172-4	Sequence 4, Appli
690	121	3.9	1139	2	US-09-513-505-4	Sequence 4, Appli	763	117.5	3.7	247	2	US-10-101-464A-730	Sequence 730, App
691	120.5	3.8	141	1	US-08-442-063A-36	Sequence 36, Appli	764	117.5	3.7	563	2	US-09-252-991A-17549	Sequence 17549, A
692	120.5	3.8	426	2	US-09-252-991A-24450	Sequence 24450, A	765	117.5	3.7	635	1	US-08-484-101B-36	Sequence 36, Appli
693	120.5	3.8	464	2	US-09-716-964B-4	Sequence 4, Appli	766	117.5	3.7	635	1	US-08-484-101B-50	Sequence 50, Appli
694	120.5	3.8	562	2	US-09-902-540-13269	Sequence 13269, A	767	117.5	3.7	635	2	US-08-714-524D-36	Sequence 36, Appli
695	120.5	3.8	787	2	US-09-721-383-2	Sequence 2, Appli	768	117.5	3.7	635	2	US-08-714-524D-50	Sequence 50, Appli
696	120.5	3.8	787	2	US-09-721-137-2	Sequence 2, Appli	769	117.5	3.7	996	2	US-10-101-464A-889	Sequence 889, App
697	120.5	3.8	787	2	US-09-721-251-2	Sequence 2, Appli	770	117.5	3.7	996	2	US-10-101-464A-933	Sequence 933, App
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700	120.5	3.8	1104	2	US-09-981-953A-4	Sequence 4, Appli	773	117.5	3.7	1706	1	US-08-399-411-2	Sequence 2, Appli
701	120.5	3.8	1587	2	US-09-949-002-354	Sequence 354, App	774	117.5	3.7	1706	2	US-08-516-859A-2	Sequence 2, Appli
702	120.5	3.8	1610	2	US-09-548-473B-4	Sequence 4, Appli	775	117.5	3.7	1706	2	US-09-586-472-2	Sequence 2, Appli
703	120.5	3.8	1665	2	US-09-858-664A-2	Sequence 2, Appli	776	117.5	3.7	1706	2	US-09-528-706-2	Sequence 2, Appli
704	120.5	3.8	1665	2	US-10-274-978-2	Sequence 2, Appli	777	117.5	3.7	1706	2	US-10-024-450-2	Sequence 2, Appli
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707	120	3.8	130	2	US-09-270-767-48303	Sequence 3086, A	780	117	3.7	655	1	US-08-448-937A-12	Sequence 12, Appli
708	120	3.8	467	2	US-09-046-736-2	Sequence 48303, A	781	117	3.7	809	2	US-09-252-991A-31759	Sequence 31759, A
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710	120	3.8	569	2	US-09-514-245-22	Sequence 22, Appli	783	117	3.7	980	1	US-08-473-553A-6	Sequence 6, Appli
711	120	3.8	603	2	US-09-906-779-4	Sequence 4, Appli	784	117	3.7	985	1	US-08-473-553A-2	Sequence 2, Appli
712	120	3.8	603	2	US-09-508-759-125	Sequence 125, App	785	117	3.7	1055	2	US-09-214-278-2	Sequence 2, Appli
713	120	3.8	2556	1	US-08-185-432-17	Sequence 17, Appli	786	117	3.7	1055	2	US-09-855-722-2	Sequence 2, Appli
714	120	3.8	2556	2	US-08-899-232-2	Sequence 2, Appli	787	117	3.7	1148	2	US-08-882-046-4	Sequence 4, Appli
715	120	3.8	2556	2	US-09-121-457-2	Sequence 2, Appli	788	117	3.7	1148	2	US-09-566-047-4	Sequence 4, Appli
716	120	3.8	520	2	US-09-107-433-3721	Sequence 3721, Ap	789	117	3.7	1193	1	US-08-400-159-10	Sequence 10, Appli
717	119.5	3.8	608	2	US-09-949-016-11148	Sequence 11148, A	790	117	3.7	1193	2	US-08-611-729A-10	Sequence 10, Appli
718	119.5	3.8	608	2	US-09-949-016-11149	Sequence 11149, A	791	117	3.7	1193	2	US-09-195-524-10	Sequence 10, Appli
719	119.5	3.8	608	2	US-09-949-016-11150	Sequence 11150, A	792	117	3.7	1193	2	US-09-310-685-8	Sequence 8, Appli
720	119.5	3.8	608	2	US-09-949-016-11151	Sequence 11151, A	793	117	3.7	1212	2	US-09-214-278-3	Sequence 3, Appli
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722	119.5	3.8	1034	2	US-09-252-991A-28921	Sequence 28921, A	795	117	3.7	1238	2	US-09-214-278-5	Sequence 5, Appli
723	119.5	3.8	1048	2	US-09-171-639-10	Sequence 10, Appli	796	117	3.7	1238	2	US-09-855-722-5	Sequence 5, Appli
724	119.5	3.8	1149	2	US-08-560-005-5	Sequence 5, Appli	797	117	3.7	1257	2	US-08-611-729A-8	Sequence 8, Appli
725	119.5	3.8	1149	2	US-09-418-540-5	Sequence 5, Appli	798	117	3.7	1257	2	US-09-195-524-8	Sequence 8, Appli
726	119.5	3.8	1149	2	US-09-969-528-5	Sequence 5, Appli	799	117	3.7	1257	2	US-09-310-685-6	Sequence 6, Appli
727	119.5	3.8	1596	2	US-09-538-092-887	Sequence 887, App	800	116.5	3.7	132	2	US-10-101-464A-572	Sequence 572, App
728	119	3.8	304	2	US-10-101-464A-717	Sequence 717, App	801	116.5	3.7	296	2	US-09-270-767-37980	Sequence 37980, A
729	119	3.8	319	2	US-08-630-172-12	Sequence 12, Appli	802	116.5	3.7	296	2	US-09-270-767-53197	Sequence 53197, A
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732	119	3.8	593	2	US-09-252-991A-20441	Sequence 20441, A	805	116.5	3.7	944	2	US-08-652-877-12	Sequence 12, Appli
733	119	3.8	784	2	US-09-982-308B-23	Sequence 23, Appli	806	116.5	3.7	1252	2	US-09-902-540-13967	Sequence 13967, A
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735	118.5	3.8	171	2	US-09-270-767-43049	Sequence 43049, A	808	116.5	3.7	4654	2	US-08-476-515A-84	Sequence 84, Appli
736	118.5	3.8	422	2	US-09-949-016-8251	Sequence 8251, Ap	809	116.5	3.7	4655	2	US-08-652-877-84	Sequence 84, Appli
737	118.5	3.8	430	2	US-09-949-016-8782	Sequence 8782, Ap	810	116.5	3.7	4655	2	US-08-652-877-86	Sequence 86, Appli
738	118.5	3.8	486	1	US-08-450-360-2	Sequence 2, Appli	811	116.5	3.7	4655	2	US-08-652-877-88	Sequence 88, Appli
739	118.5	3.8	883	2	US-10-188-495-72	Sequence 72, Appli	812	116.5	3.7	4655	2	US-08-652-877-90	Sequence 90, Appli
740	118.5	3.8	1166	2	US-10-104-047-2949	Sequence 2949, Ap	813	116	3.7	193	2	US-09-270-767-44942	Sequence 44942, A
741	118.5	3.8	1321	1	US-08-317-310A-64	Sequence 64, Appli	814	116	3.7	264	2	US-09-252-991A-24670	Sequence 24670, A
742	118	3.8	149	2	US-09-270-767-32618	Sequence 32618, A	815	116	3.7	1053	2	US-09-513-505-8	Sequence 8, Appli
743	118	3.8	149	2	US-09-270-767-47835	Sequence 47835, A	816	116	3.7	1181	2	US-09-826-509-587	Sequence 587, App
744	118	3.8	462	2	US-09-252-991A-20814	Sequence 20814, A	817	116	3.7	1291	2	US-09-150-460B-10	Sequence 10, Appli
745	118	3.8	947	2	US-09-252-991A-21335	Sequence 21335, A	818	116	3.7	1291	2	US-09-220-641-5	Sequence 5, Appli
746	118	3.8	1044	2	US-09-252-991A-18853	Sequence 18853, A	819	116	3.7	1351	2	US-09-548-473B-1	Sequence 1, Appli
747	118	3.8	1064	2	US-09-252-991A-17508	Sequence 17508, A	820	116	3.7	2556	1	US-08-083-590A-20	Sequence 20, Appli
748	118	3.8	1084	2	US-09-227-725A-3	Sequence 3, Appli	821	116	3.7	2556	1	US-08-532-384-20	Sequence 20, Appli
749	118	3.8	1084	2	US-10-071-900-3	Sequence 3, Appli	822	115.5	3.7	138	2	US-09-191-647-4	Sequence 4, Appli
750	118	3.8	1864	1	US-08-804-227C-3	Sequence 3, Appli	823	115.5	3.7	138	2	US-09-540-245A-4	Sequence 4, Appli
751	118	3.8	2471	1	US-08-185-432-16	Sequence 16, Appli	824	115.5	3.7	138	2	US-09-540-153-4	Sequence 4, Appli
752	118	3.8	2471	1	US-08-083-590A-19	Sequence 19, Appli	825	115.5	3.7	138	2	US-10-289-776-4	Sequence 4, Appli
753	118	3.8	2471	2	US-08-532-384-19	Sequence 19, Appli	826	115.5	3.7	412	2	US-09-252-991A-24484	Sequence 24484, A
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756	117.5	3.7	129	2	US-09-513-999C-4304	Sequence 4304, Ap	829	115.5	3.7	1093	4	PCT-US94-04496-55	Sequence 55, Appli
757	117.5	3.7	189	2	US-10-101-464A-517	Sequence 517, App	830	115	3.7	305	2	US-09-325-932A-188	Sequence 188, App

831	115	3.7	447	1	US-08-450-360-4	Sequence 4, Appli	904	113	3.6	681	2	US-10-362-247-2	Sequence 2, Appli
832	115	3.7	764	2	US-07-741-453A-59	Sequence 59, Appl	905	113	3.6	688	2	US-09-367-206-20	Sequence 20, Appl
833	115	3.7	764	2	US-07-741-453A-61	Sequence 61, Appl	906	113	3.6	688	2	US-09-298-404-20	Sequence 20, Appl
834	115	3.7	984	2	US-09-287-354-2	Sequence 2, Appli	907	113	3.6	723	2	US-10-104-047-2246	Sequence 2246, Ap
835	115	3.7	1053	2	US-09-513-505-6	Sequence 6, Appli	908	113	3.6	770	2	US-09-981-953A-2	Sequence 2, Appli
836	115	3.7	1093	2	US-09-252-991A-21827	Sequence 21827, A	909	113	3.6	979	2	US-09-538-092-990	Sequence 990, App
837	115	3.7	1189	2	US-09-287-354-4	Sequence 4, Appli	910	113	3.6	1247	2	US-09-501-171-6	Sequence 6, Appli
838	115	3.7	1189	2	US-09-949-016-6931	Sequence 6931, Ap	911	112.5	3.6	328	2	US-09-252-991A-17729	Sequence 17729, A
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840	115	3.7	1219	2	US-09-566-047-5	Sequence 5, Appli	913	112.5	3.6	677	1	US-08-646-715-13	Sequence 13, Appl
841	115	3.7	2415	2	US-09-949-002-398	Sequence 398, App	914	112.5	3.6	677	1	US-09-538-092-1164	Sequence 1164, Ap
842	114.5	3.7	166	2	US-09-270-767-59438	Sequence 59438, A	915	112.5	3.6	694	2	US-09-949-016-8774	Sequence 8774, Ap
843	114.5	3.7	545	2	US-09-949-002-297	Sequence 297, App	916	112.5	3.6	694	2	US-09-949-016-8775	Sequence 8775, Ap
844	114.5	3.7	545	2	US-09-509-595B-2	Sequence 2, Appli	917	112.5	3.6	711	2	US-09-949-016-8493	Sequence 8493, Ap
845	114.5	3.7	545	2	US-09-509-595B-8	Sequence 8, Appli	918	112.5	3.6	1068	1	US-08-396-479B-12	Sequence 12, Appl
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847	114.5	3.7	587	2	US-09-949-016-8709	Sequence 8709, Ap	920	112.5	3.6	1078	2	US-09-949-016-9573	Sequence 9573, Ap
848	114.5	3.7	587	2	US-09-949-002-461	Sequence 461, App	921	112	3.6	230	2	US-09-252-991A-31737	Sequence 31737, A
849	114.5	3.7	661	2	US-09-949-016-9121	Sequence 9121, Ap	922	112	3.6	241	2	US-08-341-018-54	Sequence 54, Appl
850	114.5	3.7	804	2	US-10-101-464A-890	Sequence 890, App	923	112	3.6	241	2	US-08-470-335-195	Sequence 195, App
851	114.5	3.7	935	2	US-09-902-540-16200	Sequence 16200, A	924	112	3.6	241	2	US-08-470-339-195	Sequence 195, App
852	114.5	3.7	1010	2	US-08-882-046-7	Sequence 7, Appli	925	112	3.6	241	2	US-08-467-602-389	Sequence 389, App
853	114.5	3.7	1010	2	US-09-566-047-7	Sequence 7, Appli	926	112	3.6	241	2	US-08-411-295F-47	Sequence 47, Appl
854	114.5	3.7	1017	2	US-09-600-776-6	Sequence 6, Appli	927	112	3.6	241	2	US-08-411-295F-94	Sequence 94, Appl
855	114.5	3.7	1017	2	US-09-965-830-6	Sequence 6, Appli	928	112	3.6	297	1	US-08-580-545B-6	Sequence 6, Appli
856	114.5	3.7	1036	2	US-09-068-740A-6	Sequence 6, Appli	929	112	3.6	297	1	US-09-262-545A-6	Sequence 2, Appli
857	114.5	3.7	1067	2	US-09-579-536C-18	Sequence 18, Appl	930	112	3.6	383	1	US-08-597-645-2	Sequence 2, Appli
858	114.5	3.7	1162	1	US-08-728-323A-2	Sequence 2, Appli	931	112	3.6	383	1	US-08-457-135-2	Sequence 12, Appl
859	114.5	3.7	1162	2	US-09-298-568-2	Sequence 2, Appli	932	112	3.6	383	2	US-09-142-027A-12	Sequence 11, Appl
860	114.5	3.7	1162	2	US-09-410-399-2	Sequence 2, Appli	933	112	3.6	388	2	US-09-644-858-11	Sequence 11, Appl
861	114.5	3.7	1162	2	US-09-894-273-2	Sequence 2, Appli	934	112	3.6	417	2	US-09-644-858-5	Sequence 5, Appli
862	114.5	3.7	1187	2	US-09-068-740A-7	Sequence 7, Appli	935	112	3.6	417	2	US-09-644-858-8	Sequence 8, Appli
863	114.5	3.7	1208	2	US-09-199-865-1	Sequence 1, Appli	936	112	3.6	422	2	US-09-644-858-13	Sequence 13, Appl
864	114.5	3.7	1208	2	US-10-213-329-1	Sequence 1, Appli	937	112	3.6	479	2	US-09-252-991A-23144	Sequence 23144, A
865	114.5	3.7	1218	1	US-08-400-159-6	Sequence 6, Appli	938	112	3.6	513	1	US-08-480-229C-14	Sequence 14, Appl
866	114.5	3.7	1218	2	US-08-611-729A-6	Sequence 6, Appli	939	112	3.6	513	1	US-08-659-235C-14	Sequence 14, Appl
867	114.5	3.7	1218	2	US-08-882-046-2	Sequence 2, Appli	940	112	3.6	720	2	US-09-252-991A-31915	Sequence 31915, A
868	114.5	3.7	1218	2	US-09-068-740A-11	Sequence 11, Appl	941	112	3.6	750	2	US-09-165-239A-4	Sequence 4, Appli
869	114.5	3.7	1218	2	US-09-566-047-2	Sequence 2, Appli	942	112	3.6	764	2	US-07-757-342D-5	Sequence 5, Appli
870	114.5	3.7	1218	2	US-09-917-254-85	Sequence 85, Appl	943	112	3.6	764	2	US-09-451-657B-5	Sequence 5, Appli
871	114.5	3.7	1218	2	US-09-195-524-6	Sequence 6, Appli	944	112	3.6	764	2	US-09-826-509-395	Sequence 395, App
872	114.5	3.7	1218	2	US-09-579-536C-1	Sequence 1, Appli	945	112	3.6	764	2	US-09-826-509-399	Sequence 399, App
873	114.5	3.7	1218	2	US-09-949-016-5902	Sequence 5902, Ap	946	112	3.6	764	2	US-09-826-509-403	Sequence 403, App
874	114.5	3.7	1218	2	US-09-310-685-4	Sequence 4, Appli	947	112	3.6	764	2	US-09-826-509-407	Sequence 407, App
875	114.5	3.7	1254	2	US-09-949-016-10297	Sequence 10297, A	948	112	3.6	764	2	US-09-826-509-411	Sequence 411, App
876	114.5	3.7	2169	2	US-09-949-016-6930	Sequence 6930, Ap	949	112	3.6	764	2	US-09-826-509-415	Sequence 415, App
877	114	3.6	111	2	US-09-220-528-33	Sequence 53, Appl	950	112	3.6	764	2	US-09-826-509-419	Sequence 419, App
878	114	3.6	224	2	US-09-220-528-29	Sequence 29, Appl	951	112	3.6	764	2	US-09-826-509-423	Sequence 423, App
879	114	3.6	224	2	US-09-347-613C-16	Sequence 16, Appl	952	112	3.6	902	1	US-08-396-479B-6	Sequence 6, Appli
880	114	3.6	224	2	US-09-662-183A-16	Sequence 16, Appl	953	112	3.6	902	1	US-08-818-823-6	Sequence 6, Appli
881	114	3.6	257	2	US-10-101-464A-743	Sequence 743, App	954	112	3.6	990	2	US-10-101-464A-814	Sequence 814, App
882	114	3.6	497	2	US-10-104-047-3773	Sequence 3773, Ap	955	112	3.6	1833	2	US-08-479-722B-2	Sequence 2, Appli
883	114	3.6	631	2	US-08-270-767-4123	Sequence 4123, A	956	112	3.6	1833	2	US-09-592-685-2	Sequence 2, Appli
884	114	3.6	644	1	US-08-866-757-2	Sequence 2, Appli	957	112	3.6	1833	4	PCT-US95-02251-18	Sequence 18, Appl
885	114	3.6	644	2	US-09-153-593-2	Sequence 2, Appli	958	111.5	3.6	228	2	US-09-902-540-15349	Sequence 15349, A
886	114	3.6	681	2	US-10-104-047-3586	Sequence 3586, Ap	959	111.5	3.6	281	2	US-09-252-991A-23962	Sequence 23962, A
887	114	3.6	875	2	US-09-150-460B-7	Sequence 7, Appli	960	111.5	3.6	281	2	US-10-101-464A-619	Sequence 619, App
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889	114	3.6	1063	1	US-08-127-499A-8	Sequence 8, Appli	962	111.5	3.6	417	2	US-09-949-016-11097	Sequence 11097, A
890	114	3.6	1063	1	US-08-482-847-8	Sequence 8, Appli	963	111.5	3.6	417	2	US-09-949-016-11098	Sequence 11098, A
891	114	3.6	1065	1	US-08-400-159-8	Sequence 8, Appli	964	111.5	3.6	417	2	US-09-949-002-548	Sequence 548, App
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893	114	3.6	3571	2	US-09-911-842A-2	Sequence 2, Appli	966	111.5	3.6	766	2	US-09-902-540-10602	Sequence 10602, A
894	114	3.6	3597	2	US-10-037-417-6	Sequence 6, Appli	967	111.5	3.6	816	2	US-09-266-225D-12	Sequence 12, Appl
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896	113.5	3.6	240	2	US-09-689-486-61	Sequence 61, Appl	969	111.5	3.6	1021	2	US-10-101-464A-954	Sequence 954, App
897	113.5	3.6	685	2	US-10-101-464A-918	Sequence 918, App	970	111.5	3.6	1298	1	US-08-690-473-2	Sequence 2, Appli
898	113.5	3.6	841	2	US-09-252-991A-26919	Sequence 26919, A	971	111.5	3.6	1298	2	US-09-259-821A-2	Sequence 2, Appli
899	113.5	3.6	1164	2	US-09-902-540-12627	Sequence 12627, A	972	111.5	3.6	1298	2	US-08-843-659-2	Sequence 2, Appli
900	113.5	3.6	1218	2	US-09-214-278-7	Sequence 7, Appli	973	111.5	3.6	1298	2	US-09-825-288A-2	Sequence 2, Appli
901	113.5	3.6	1218	2	US-09-855-722-7	Sequence 7, Appli	974	111	3.5	239	2	US-09-252-991A-21250	Sequence 21250, A
902	113	3.6	175	2	US-10-101-464A-801	Sequence 801, App	975	111	3.5	267	2	US-08-818-112-142	Sequence 112, App
903	113	3.6	369	2	US-09-252-991A-25394	Sequence 25394, A	976	111	3.5	267	2	US-08-818-111-137	Sequence 137, App

977	111	3.5	267	2	US-09-056-556-142	Sequence 142, App	1050	109.5	3.5	297	2	US-09-252-991A-32590	Sequence 32590, A
978	111	3.5	267	2	US-09-072-596-137	Sequence 137, App	1051	109.5	3.5	343	2	US-10-101-464A-892	Sequence 892, App
979	111	3.5	267	2	US-09-072-967-112	Sequence 142, App	1052	109.5	3.5	381	2	US-10-101-464A-660	Sequence 660, App
980	111	3.5	267	2	US-10-193-002-137	Sequence 137, App	1053	109.5	3.5	400	2	US-10-101-464A-939	Sequence 939, App
981	111	3.5	267	2	US-10-084-843-142	Sequence 142, App	1054	109.5	3.5	401	6	5252556-1	Patent No. 5252556
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983	111	3.5	333	2	US-09-253-991A-19956	Sequence 19956, A	1056	109.5	3.5	456	2	US-08-467-602-303	Sequence 303, App
984	111	3.5	452	2	US-09-949-016-7289	Sequence 7289, App	1057	109.5	3.5	456	2	US-08-411-295F-229	Sequence 229, App
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986	111	3.5	492	1	US-08-644-271-32	Sequence 32, App	1059	109.5	3.5	490	2	US-08-411-295F-271	Sequence 271, App
987	111	3.5	492	1	US-09-077-965-36	Sequence 36, App	1060	109.5	3.5	612	1	US-08-359-705B-8	Sequence 8, Appl
988	111	3.5	492	2	US-10-016-283-36	Sequence 36, Appl	1061	109.5	3.5	612	1	US-08-286-846A-8	Sequence 8, Appl
989	111	3.5	595	2	US-09-949-016-7205	Sequence 7205, App	1062	109.5	3.5	612	1	US-08-457-880A-8	Sequence 8, Appl
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991	111	3.5	699	2	US-09-461-657B-2	Sequence 2, Appl	1064	109.5	3.5	612	2	US-08-942-562-8	Sequence 8, Appl
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995	111	3.5	1318	2	US-10-237-551-197	Sequence 197, App	1068	109.5	3.5	690	2	US-10-101-464A-69	Sequence 69, Appl
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997	111	3.5	1358	1	US-08-404-671-4	Sequence 4, Appl	1070	109.5	3.5	697	2	US-10-101-464A-940	Sequence 940, App
998	111	3.5	1358	1	US-08-404-781-4	Sequence 4, Appl	1071	109.5	3.5	784	2	US-09-004-838-12	Sequence 12, Appl
999	111	3.5	1540	2	US-09-949-016-11382	Sequence 4, Appl	1072	109.5	3.5	784	2	US-09-150-460B-8	Sequence 8, Appl
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1002	111	3.5	1719	1	US-08-459-568-4	Sequence 4, Appl	1075	109.5	3.5	839	1	US-08-457-880A-6	Sequence 6, Appl
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1004	111	3.5	1719	1	US-08-516-859A-4	Sequence 4, Appl	1077	109.5	3.5	839	2	US-08-942-562-6	Sequence 6, Appl
1005	111	3.5	1719	2	US-09-586-472-4	Sequence 4, Appl	1078	109.5	3.5	839	2	US-09-156-923-6	Sequence 6, Appl
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1008	111	3.5	2254	2	US-09-949-016-9270	Sequence 9270, App	1081	109.5	3.5	1235	2	US-09-949-016-8456	Sequence 8456, App
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1010	111	3.5	2442	2	US-09-538-092-1370	Sequence 1370, App	1083	109	3.5	221	1	US-08-480-229C-29	Sequence 29, Appl
1011	111	3.5	2523	1	US-08-185-432-18	Sequence 18, Appl	1084	109	3.5	221	1	US-08-659-235C-29	Sequence 29, Appl
1012	111	3.5	2523	2	US-08-899-232-3	Sequence 3, Appl	1085	109	3.5	416	2	US-08-978-289-12	Sequence 12, Appl
1013	111	3.5	2523	2	US-09-121-457-3	Sequence 3, Appl	1086	109	3.5	416	2	US-09-601-478-1	Sequence 1, Appl
1014	110.5	3.5	273	2	US-09-252-991A-30433	Sequence 30433, A	1087	109	3.5	416	2	US-09-601-478-4	Sequence 4, Appl
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1016	110.5	3.5	565	2	US-08-937-067-8	Sequence 8, Appl	1089	109	3.5	437	1	US-08-136-119-2	Sequence 2, Appl
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1018	110.5	3.5	675	2	US-09-332-063-2	Sequence 2, Appl	1091	109	3.5	439	2	US-09-252-991A-32620	Sequence 32620, A
1019	110.5	3.5	675	2	US-09-332-063-3	Sequence 3, Appl	1092	109	3.5	447	2	US-09-949-002-540	Sequence 540, App
1020	110.5	3.5	708	2	US-09-818-780-76	Sequence 76, Appl	1093	109	3.5	480	1	US-08-480-229C-10	Sequence 10, Appl
1021	110.5	3.5	728	2	US-09-252-991A-31891	Sequence 31891, A	1094	109	3.5	480	1	US-08-659-235C-10	Sequence 24, Appl
1022	110.5	3.5	815	2	US-09-538-092-1300	Sequence 1300, App	1095	109	3.5	507	2	US-09-599-287A-24	Sequence 24, Appl
1023	110.5	3.5	1207	2	US-10-098-600B-16	Sequence 16, App	1096	109	3.5	510	2	US-10-078-547-24	Sequence 24, Appl
1024	110.5	3.5	1346	2	US-09-949-002-376	Sequence 376, App	1097	109	3.5	552	2	US-09-252-991A-23036	Sequence 23036, A
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1026	110.5	3.5	1346	2	US-09-105-537-37	Sequence 37, Appl	1099	109	3.5	560	2	US-09-252-991A-25999	Sequence 25999, A
1027	110.5	3.5	1346	2	US-09-141-908-5	Sequence 5, Appl	1100	109	3.5	749	2	US-08-828-313-27	Sequence 27, Appl
1028	110.5	3.5	1346	2	US-09-657-440-4	Sequence 4, Appl	1101	109	3.5	762	1	US-08-642-255-114	Sequence 114, App
1029	110.5	3.5	1346	2	US-09-793-708-4	Sequence 4, Appl	1102	109	3.5	762	1	US-08-397-633A-26	Sequence 26, Appl
1030	110.5	3.5	1384	2	US-08-976-255-11	Sequence 11, Appl	1103	109	3.5	764	2	US-09-186-350A-53	Sequence 53, Appl
1031	110.5	3.5	1656	1	US-09-949-016-7247	Sequence 7247, App	1104	109	3.5	828	2	US-10-101-464A-934	Sequence 934, App
1032	110.5	3.5	2476	1	US-08-276-967-2	Sequence 2, Appl	1105	109	3.5	833	1	US-08-264-534-6	Sequence 6, Appl
1033	110.5	3.5	3724	1	US-08-804-227C-10	Sequence 10, Appl	1106	109	3.5	833	1	US-08-083-590A-2	Sequence 2, Appl
1034	110.5	3.5	3724	1	US-08-804-198-4	Sequence 4, Appl	1107	109	3.5	833	1	US-08-465-500-6	Sequence 6, Appl
1035	110.5	3.5	11877	2	US-09-105-537-6	Sequence 6, Appl	1108	109	3.5	833	1	US-08-346-126-6	Sequence 6, Appl
1036	110	3.5	195	2	US-09-858-664A-11	Sequence 11, Appl	1109	109	3.5	833	1	US-08-532-384-2	Sequence 2, Appl
1037	110	3.5	195	2	US-10-274-978-12	Sequence 12, Appl	1110	109	3.5	833	2	US-08-893-828-6	Sequence 6, Appl
1038	110	3.5	195	2	US-10-697-263-12	Sequence 12, Appl	1111	109	3.5	833	2	US-08-286-305A-7	Sequence 7, Appl
1039	110	3.5	450	2	US-09-369-364A-19	Sequence 19, App	1112	109	3.5	850	1	US-08-441-104A-7	Sequence 7, Appl
1040	110	3.5	626	2	US-09-345-473E-43	Sequence 43, App	1113	109	3.5	850	1	US-08-440-816A-7	Sequence 7, Appl
1041	110	3.5	626	2	US-09-862-027-43	Sequence 43, Appl	1114	109	3.5	850	2	US-09-417-381A-7	Sequence 7, Appl
1042	110	3.5	633	2	US-09-248-796A-18023	Sequence 18023, A	1115	109	3.5	850	2	US-09-252-991A-28607	Sequence 28607, A
1043	110	3.5	739	2	US-09-035-648-24	Sequence 24, Appl	1116	109	3.5	860	2	US-10-195-970-3	Sequence 3, Appl
1044	110	3.5	739	2	US-09-001-951-24	Sequence 24, Appl	1117	109	3.5	883	2	US-10-195-970-6	Sequence 6, Appl
1045	110	3.5	739	2	US-08-818-823-24	Sequence 24, Appl	1118	109	3.5	883	2	US-08-758-759-167	Sequence 167, App
1046	110	3.5	746	2	US-09-548-797B-4	Sequence 4, Appl	1119	109	3.5	1145	2	US-08-231-193A-58	Sequence 58, Appl
1047	110	3.5	2703	1	US-08-185-432-19	Sequence 19, App	1120	109	3.5	1336	1	US-08-486-273A-58	Sequence 58, Appl
1048	110	3.5	2703	2	US-08-899-232-4	Sequence 4, Appl	1121	109	3.5	1336	1	US-08-940-086A-58	Sequence 58, Appl
1049	110	3.5	2703	2	US-09-121-457-4	Sequence 4, Appl	1122	109	3.5	1336	2		

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1124	109	3.5	1336	2	US-08-935-105A-58	Sequence 58, Appl	1197	107.5	3.4	493	2	US-08-467-602-341	Sequence 341, App
1125	109	3.5	1336	2	US-09-648-797-58	Sequence 58, Appl	1198	107.5	3.4	493	2	US-08-411-295F-267	Sequence 267, App
1126	109	3.5	1336	2	US-09-386-123-58	Sequence 58, Appl	1199	107.5	3.4	506	2	US-09-949-016-11282	Sequence 11282, A
1127	109	3.5	1336	2	US-10-038-937-58	Sequence 58, Appl	1200	107.5	3.4	520	2	US-09-068-740A-3	Sequence 3, Appl
1128	109	3.5	1336	2	US-10-007-747-58	Sequence 58, Appl	1201	107.5	3.4	568	2	US-09-252-991A-19968	Sequence 19968, A
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1130	109	3.5	1358	2	US-09-949-002-353	Sequence 353, App	1203	107.5	3.4	660	2	US-10-101-464A-808	Sequence 808, App
1131	109	3.5	1385	2	US-09-949-002-431	Sequence 431, App	1204	107.5	3.4	691	2	US-09-252-991A-31413	Sequence 31413, A
1132	108.5	3.5	74	2	US-09-270-767-32762	Sequence 32762, A	1205	107.5	3.4	691	2	US-09-758-759-159	Sequence 159, App
1133	108.5	3.5	74	2	US-09-270-767-47979	Sequence 47979, A	1206	107.5	3.4	723	2	US-09-641-612-6	Sequence 6, Appl
1134	108.5	3.5	269	2	US-09-902-540-16596	Sequence 16596, A	1207	107.5	3.4	782	2	US-09-252-991A-19991	Sequence 19991, A
1135	108.5	3.5	288	2	US-08-902-540-16596	Sequence 16596, A	1208	107.5	3.4	832	2	US-08-981-392-6	Sequence 6, Appl
1136	108.5	3.5	381	2	US-09-510-031A-5	Sequence 5, Appl	1209	107.5	3.4	832	2	US-09-908-322-6	Sequence 6, Appl
1137	108.5	3.5	404	2	US-09-550-111A-11	Sequence 11, Appl	1210	107.5	3.4	984	1	US-08-673-789-9	Sequence 9, Appl
1138	108.5	3.5	514	2	US-09-712-363-154	Sequence 154, App	1211	107.5	3.4	998	2	US-09-949-016-6695	Sequence 6695, Ap
1139	108.5	3.5	542	2	US-09-252-991A-21862	Sequence 21862, A	1212	107.5	3.4	1001	2	US-10-415-147-3	Sequence 3, Appl
1140	108.5	3.5	548	1	US-08-468-576B-19	Sequence 19, Appl	1213	107.5	3.4	1088	2	US-09-233-857-13	Sequence 13, Appl
1141	108.5	3.5	548	1	US-08-468-579B-19	Sequence 19, Appl	1214	107.5	3.4	1135	1	US-08-574-959A-7	Sequence 7, Appl
1142	108.5	3.5	548	2	US-08-468-579B-19	Sequence 19, Appl	1215	107.5	3.4	1135	2	US-09-357-014-7	Sequence 7, Appl
1143	108.5	3.5	702	2	US-09-068-740A-4	Sequence 4, Appl	1216	107.5	3.4	1327	2	US-09-949-016-8412	Sequence 8412, Ap
1144	108.5	3.5	723	2	US-09-068-740A-9	Sequence 9, Appl	1217	107	3.4	131	1	US-08-650-598-3	Sequence 3, Appl
1145	108.5	3.5	723	2	US-09-423-753-27	Sequence 27, Appl	1218	107	3.4	232	2	US-09-149-476-623	Sequence 623, App
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1147	108.5	3.5	827	2	US-09-248-796A-17307	Sequence 17307, A	1220	107	3.4	354	2	US-09-949-016-6051	Sequence 6051, Ap
1148	108.5	3.5	904	2	US-09-252-991A-23202	Sequence 23202, A	1221	107	3.4	358	2	US-09-949-016-8148	Sequence 8148, Ap
1149	108.5	3.5	955	2	US-09-252-991A-24254	Sequence 24254, A	1222	107	3.4	360	2	US-09-248-796A-18991	Sequence 18991, A
1150	108.5	3.5	1125	2	US-09-513-783A-152	Sequence 152, App	1223	107	3.4	369	2	US-09-252-991A-29670	Sequence 29670, A
1151	108.5	3.5	1125	2	US-09-430-656-152	Sequence 152, App	1224	107	3.4	492	2	US-09-252-991A-23619	Sequence 23619, A
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1153	108.5	3.5	1184	2	US-09-286-225D-18	Sequence 18, Appl	1226	107	3.4	541	2	US-10-101-464A-913	Sequence 913, App
1154	108.5	3.5	1527	2	US-09-695-795A-4	Sequence 4, Appl	1227	107	3.4	593	2	US-09-964-899-15	Sequence 15, Appl
1155	108.5	3.5	1610	2	US-09-513-783A-22	Sequence 22, Appl	1228	107	3.4	615	2	US-09-949-002-301	Sequence 301, App
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1161	108	3.4	180	2	US-09-133-341-12	Sequence 12, Appl	1234	107	3.4	1315	2	US-08-899-595-3	Sequence 3, Appl
1162	108	3.4	180	2	US-09-739-852-12	Sequence 12, Appl	1235	106.5	3.4	157	2	US-08-981-392-68	Sequence 68, Appl
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1186	107.5	3.4	134	2	US-09-540-245A-12	Sequence 12, Appl	1259	106.5	3.4	1185	2	US-09-041-886-23	Sequence 23, Appl
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1284	106	3.4	1209	2	US-09-949-002-494	Sequence 494, App	1357	106	3.4	2322	2	US-10-010-720-34	Sequence 34, Appl
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1287	106	3.4	1214	2	US-08-480-474-54	Sequence 54, Appl	1360	106	3.4	2743	2	US-10-037-182-36	Sequence 36, Appl
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1319	106	3.4	1236	1	US-08-486-273A-6	Sequence 6, Appl	1392	105	3.3	196	2	US-09-908-322-35	Sequence 325, App
1320	106	3.4	1236	2	US-08-480-474-6	Sequence 6, Appl	1393	105	3.3	254	2	US-09-199-637A-325	Sequence 325, App
1321	106	3.4	1236	2	US-08-940-086A-6	Sequence 6, Appl	1394	105	3.3	422	2	US-09-151-102-2	Sequence 2, Appl
1322	106	3.4	1236	2	US-08-940-035A-6	Sequence 6, Appl	1395	105	3.3	422	2	US-08-929-846-2	Sequence 2, Appl
1323	106	3.4	1236	2	US-08-935-105A-6	Sequence 6, Appl	1396	105	3.3	422	2	US-08-663-584-2	Sequence 2, Appl
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1340	106	3.4	1244	1	US-08-231-193A-46	Sequence 46, Appl	1413	105	3.3	895	1	US-08-483-278-8	Sequence 8, Appl
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Db 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQRPNATYSVCVNPGLPGRVPEGEACGAHT 480
Qy 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLLAAVGAAYCVRRGRAMAAQAQDKGV 540
Db 481 PPAVSHNAPVTQAREGNLPLLIAPALAAVLLAAVGAAYCVRRGRAMAAQAQDKGV 540
Qy 541 GPGAGPLEGVKVPLEPGPKATGEGGALPSGSECEVPLMGFPGLQSPHAKPYI 598
Db 541 GPGAGPLEGVKVPLEPGPKATGEGGALPSGSECEVPLMGFPGLQSPHAKPYI 598

RESULT 2

US-09-944-457-69
; Sequence 69, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944, 457
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067, 411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069, 696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069, 873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068, 017

; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070, 440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074, 086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074, 092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075, 945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112, 850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113, 296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146, 222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216, 021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218, 517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254, 311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-69

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MCSRVPLLLPLLLLLALGPGVQGCFCGCGCQSQPOTVCTARQGTTPRDPVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLLALGPGVQGCFCGCGCQSQPOTVCTARQGTTPRDPVPPDTVGLYVF 60
Qy 61 ENGITMLDASSFAGLPGQLLLDLSQNQIASURLPRLLLDLSHNSLLALEPGILD TANVE 120
Db 61 ENGITMLDASSFAGLPGQLLLDLSQNQIASURLPRLLLDLSHNSLLALEPGILD TANVE 120
Qy 121 ALRLAGLQQLDDEGLFSRLNHLHDLDVSDNQLRVPVIRGLRGLTRLRLAGNTRIAQL 180


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Db      1 MCSRVPLLLPLLLALLLGGVQGCSPGCCQSQPQVTFCTARQGTTPVDPDVTGLVYVF 60
Qy      61 ENGTMLDASSFAGLPGLQLDLSONQIASLRPLRLLLLDLSHNSLLALEPGILDANVE 120
Db      61 ENGTMLDASSFAGLPGLQLDLSONQIASLRPLRLLLLDLSHNSLLALEPGILDANVE 120
Qy     121 ALRLAGLQLODDEGLFSRLNHLHDLVSDNQLERVPVPIGLRGLTFLRLAGNTRIAQL 180
Db     121 ALRLAGLQLODDEGLFSRLNHLHDLVSDNQLERVPVPIGLRGLTFLRLAGNTRIAQL 180
Qy     181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLILAAARNPNCVPLSWFGPWVRE 240
Db     181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLILAAARNPNCVPLSWFGPWVRE 240
Qy     241 SHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVTPTRPVVREPTALSSSL 300
Db     241 SHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVTPTRPVVREPTALSSSL 300
Qy     301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPBG 360
Db     301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGTCHLGRHHLACLCPBG 360
Qy     361 FTGLYCESQMGQGRPSPTVTPRPSRLTLGIEPVSTSLRVGLQRYLQSSVQLRSRLR 420
Db     361 FTGLYCESQMGQGRPSPTVTPRPSRLTLGIEPVSTSLRVGLQRYLQSSVQLRSRLR 420
Qy     421 LTYRNLSPDKRLVTLRLPASLAETVTTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
Db     421 LTYRNLSPDKRLVTLRLPASLAETVTTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
Qy     481 PPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAADQKGV 540
Db     481 PPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAADQKGV 540
Qy     541 GPGAGPLEGVKVPLEPGPKATEGGREALPGSGSECVPLMGFPQPGQLQSPHLHAKPYI 598
Db     541 GPGAGPLEGVKVPLEPGPKATEGGREALPGSGSECVPLMGFPQPGQLQSPHLHAKPYI 598

RESULT 4
US-09-944-944-69
; Sequence 69, Application US/09944944
; Patent No.. 6929947
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866, 028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067, 411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069, 334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069, 425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069, 696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069, 870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069, 873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068, 017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070, 440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074, 086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074, 092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075, 945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112, 850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113, 296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146, 222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216, 021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218, 517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254, 311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
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; ORGANISM: Homo Sapien
US-09-944-944-69

Query Match      100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCSRVPLLLPLLLALLGPGVGGQSPGSCQSQPQTVCCTARQGTTPRDPVPPDTVGLYVF 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 1 MCSRVPLLLPLLLALLGPGVGGQSPGSCQSQPQTVCCTARQGTTPRDPVPPDTVGLYVF 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 ENGLTMDASSFAGLGLQLDLSONQIASRLRLLLLDLSHNSILALEPGILDITANVE 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 61 ENGLTMDASSFAGLGLQLDLSONQIASRLRLLLLDLSHNSILALEPGILDITANVE 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 ALRLAGLQQLDGLFSRLNHLHDVSDNQLSERVPPVIRGLRGLTRLRLAGNTRIAQL 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 121 ALRLAGLQQLDGLFSRLNHLHDVSDNQLSERVPPVIRGLRGLTRLRLAGNTRIAQL 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 RPEDLAGLAALQELDVSNLSLQALPGDLISGLFPRLRLLAARNPNCVPLSNWFGPWVRE 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 181 RPEDLAGLAALQELDVSNLSLQALPGDLISGLFPRLRLLAARNPNCVPLSNWFGPWVRE 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVTPTRPVVREPTALSSSL 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVTPTRPVVREPTALSSSL 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCHLGRHHLACLCEG 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCHLGRHHLACLCEG 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 361 FTGLYCSQMGQGRPSPTPTVTPRPRSLTLGIEFVSPTSIRVLQRYLQSSSVQLRSRLR 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 361 FTGLYCSQMGQGRPSPTPTVTPRPRSLTLGIEFVSPTSIRVLQRYLQSSSVQLRSRLR 420
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 421 LTYRNLSPDKRLVTLRLPASLAETVTLQPNATYSVCMPLGPGRVPEGEERACGEAHT 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 421 LTYRNLSPDKRLVTLRLPASLAETVTLQPNATYSVCMPLGPGRVPEGEERACGEAHT 480
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 481 PPAVSHNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRMAAAQAQDKGV 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 481 PPAVSHNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRMAAAQAQDKGV 540
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 541 GPGAGPLEGKVKPLBPGPKATGSGGEALPSGSECEVPLMGFGPGGLQSPPLHAKPYI 598
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 541 GPGAGPLEGKVKPLBPGPKATGSGGEALPSGSECEVPLMGFGPGGLQSPPLHAKPYI 598
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-09-945-587-69
; Sequence 69, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69

Query Match 100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGPGVQGCPCSCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
DB 1 MCSRVPLLLPLLLLLALGPGVQGCPCSCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60

QY 61 ENGITMLDASSFAGLPGQLDLSONQIASRLRLLILLDLSHNSLLALEPGILDANVE 120
DB 61 ENGITMLDASSFAGLPGQLDLSONQIASRLRLLILLDLSHNSLLALEPGILDANVE 120

QY 121 ALRLAGLGLQQLDEGLFSLRNLHDLVDSDNQLERVPVIRGLRGLTRLRAGNTRIAQL 180
DB 121 ALRLAGLGLQQLDEGLFSLRNLHDLVDSDNQLERVPVIRGLRGLTRLRAGNTRIAQL 180

QY 181 RPEDLAGLAAQLQELDVSNLSLQALPGDLGSLFPRLRLAAARNPNCVCLPSWFGPWVRE 240
DB 181 RPEDLAGLAAQLQELDVSNLSLQALPGDLGSLFPRLRLAAARNPNCVCLPSWFGPWVRE 240

QY 241 SHVTLASPEETRCHFPKQAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
DB 241 SHVTLASPEETRCHFPKQAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300

QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPDQCPSPCLNGGTCCHLGRHHLACLCEPG 360
DB 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPDQCPSPCLNGGTCCHLGRHHLACLCEPG 360

QY 361 FTGLYCESQMGQGTTPVTPRPSRLTLGIEPVSPTSRLVQLQRYLGSSVQLRSRLR 420
DB 361 FTGLYCESQMGQGTTPVTPRPSRLTLGIEPVSPTSRLVQLQRYLGSSVQLRSRLR 420

QY 421 LTYRNLSPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPLGGRVPEGEACGEAHT 480
DB 421 LTYRNLSPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPLGGRVPEGEACGEAHT 480

QY 481 PPAVHSHNAPVTQAREGNPLPPIALPALAAVLLAALAAVGAAYCVRGRAMAQAQDKGV 540
DB 481 PPAVHSHNAPVTQAREGNPLPPIALPALAAVLLAALAAVGAAYCVRGRAMAQAQDKGV 540

QY 541 GPGAGPLEGVKVPLEPGPKATEGGALPGSGSECEVPLMGFPGLQSPHAKPYI 598
DB 541 GPGAGPLEGVKVPLEPGPKATEGGALPGSGSECEVPLMGFPGLQSPHAKPYI 598

RESULT 6
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; CURRENT FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-063-950-2
Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLLPLLLLLALGPGVQGCPCSCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60
DB 1 MCSRVPLLLPLLLLLALGPGVQGCPCSCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60

QY 61 ENGITMLDASSFAGLPGQLDLSONQIAS-----LRLPRLILLDLSHNS 90
DB 61 ENGITMLDASSFAGLPGQLDLSONQIASLPSGVFQPLANLSNLDLTANRHLHEITNETF 120

QY 91 -----LRLPRLILLDLSHNS 105
DB 91 -----LRLPRLILLDLSHNS 180

QY 106 LLALEPGILDANVEALRLAGLQQLDEGLFSLRNLHDLVDSDNQLERVPVIRGLRG 165
DB 106 LLALEPGILDANVEALRLAGLQQLDEGLFSLRNLHDLVDSDNQLERVPVIRGLRG 240

QY 166 LTRLRAGNTRIAQLRPEDLAGLAAQLQELDVSNLSLQALPGDLGSLFPRLRLAAARNPF 225
DB 166 LTRLRAGNTRIAQLRPEDLAGLAAQLQELDVSNLSLQALPGDLGSLFPRLRLAAARNPF 300

QY 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKQAGRLLELDYADFGCPATTTTATVPT 285
DB 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKQAGRLLELDYADFGCPATTTTATVPT 360

QY 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVQPDQCPSPCLNGGTC 345
DB 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVQPDQCPSPCLNGGTC 420

QY 346 HLGRHHLACLCPGFTGLYCESQMGQGTTPVTPRPSRLTLGIEPVSPTSRLVGL 405
DB 346 HLGRHHLACLCPGFTGLYCESQMGQGTTPVTPRPSRLTLGIEPVSPTSRLVGL 480

QY 406 QRYLQSSVQLRSRLTYRNLSPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPLGP 465
DB 406 QRYLQSSVQLRSRLTYRNLSPDKRLVTLRLPASLAETVTLQRPNATYSVCVMPLGP 540

QY 466 GRVPEGEACGEAHTPPAVHSHNAPVTQAREGNPLPPIALPALAAVLLAALAAVGAAYCVR 525
DB 466 GRVPEGEACGEAHTPPAVHSHNAPVTQAREGNPLPPIALPALAAVLLAALAAVGAAYCVR 600

QY 526 RGRMAAAAQDKGVQGFAGGLEGVKVPLEPGPKATEGGALPGSGSECEVPLMGFP 585
DB 526 RGRMAAAAQDKGVQGFAGGLEGVKVPLEPGPKATEGGALPGSGSECEVPLMGFP 660

QY 586 PGLOSPLHAKPYI 598
DB 586 PGLOSPLHAKPYI 673

RESULT 7
US-09-991-181-52
; Sequence 52, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.	PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James	PRIOR FILING DATE: 1998-06-10
APPLICANT: Paoni, Nicholas F.	PRIOR APPLICATION NUMBER: 60/088810
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/088824
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088826
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088858
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	PRIOR APPLICATION NUMBER: 60/088861
TITLE OF INVENTION: Acids Encoding the Same	PRIOR FILING DATE: 1998-06-11
FILE REFERENCE: P2730PIC53	PRIOR APPLICATION NUMBER: 60/088876
CURRENT APPLICATION NUMBER: US/09/991,181	PRIOR FILING DATE: 1998-06-11
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34 PRIOR FILING DATE: 1998-07-07
35 PRIOR APPLICATION NUMBER: 60/091982
36 PRIOR FILING DATE: 1998-07-07
37 PRIOR APPLICATION NUMBER: 60/092182
38 PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
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Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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DB 61 ENGITMLDAGSFAGLPGQLLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120
QY 91 -----LRLPRLLLLLSHNS 105
DB 121 RGLRRRLRYLGNRIHQPCAFPTDLRLLEKLQDNELRALPPLRLPRLLLLLSHNS 180
QY 106 LLALRPGILDTANVRLKAGLGQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG 165
DB 181 LLALRPGILDTANVRLKAGLGQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG 240
QY 166 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLPRLRLAARNPF 225
DB 241 LTRRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLPRLRLAARNPF 300
QY 226 NCVCPLSWFGPWRESHVTLASPEETRCHFFPKNAGRLLELDYADFQCPATTTTATVPT 285
DB 301 NCVCPLSWFGPWRESHVTLASPEETRCHFFPKNAGRLLELDYADFQCPATTTTATVPT 360
QY 286 TRPVVREPTALSSSLAPTWLSFTAPATEAPSPPTAPTVGPVQPCPPESTCLNGGTC 345
DB 361 TRPVVREPTALSSSLAPTWLSFTAPATEAPSPPTAPTVGPVQPCPPESTCLNGGTC 420
QY 346 HLGTRHHLACLCEGFTGLCYESQMGQGTTRPPTVTPRPRSLTLGIEPVSPSLRVGL 405

DB 421 HLGTRHHLACLCEGFTGLCYESQMGQGTTRPPTVTPRPRSLTLGIEPVSPSLRVGL 480
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DB 481 QRYLQSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAETVTTQLRPNATYSVCVMPGLP 540
QY 466 GRVPEGEACGEAHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
DB 541 GRVPEGEACGEAHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600
QY 526 RGRAMAAAADKQGVGFCAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPG 585
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DB 661 PGLQSPHLHAKPYI 673

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; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730FIC19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-05-07
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76	PRIOR APPLICATION NUMBER: 60/091978
77	PRIOR FILING DATE: 1998-07-07
78	PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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QY 91 -----LRLPRLLLDLSHNS 105
Dd 121 RGLRRLERLYLGNKRIRHQPAGFDTDLRLLEKLQDNELRALPFLRLPRLLLDLSHNS 180
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Dd 181 LLALEPGILTANVEALRAGLGLQQLDEGLFSRLRNLDLVDSDNQLERVPVIRGLRG 240
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
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; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540

; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;

Best Local Similarity 88.7%; Pred. No. 3.8e-213;

Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

Qy 1 MCSRVPLLLPLLLLLALGPGVQCPCSCQCSQPTVCTARQGTTPRDVPPDTVGLXVF 60
Db 1 MCSRVPLLLPLLLLLALGPGVQCPCSCQCSQPTVCTARQGTTPRDVPPDTVGLXVF 60
Qy 61 ENGITMLDASSFAGLPGLQLDLDSQNIAS----- 90
Db 61 ENGITMLDAGSFAGLPGLQLDLDSQNIASLPSGVGFQPLANLSNLDLTANRLHEITNETFF 120
Qy 91 -----LRLPRLLLLDLSHNS 105
Db 121 RGLRLRLYLGKNNRIRHIQFGAPDTLDRLELKLQNELRALPPLRLPRLLLDLSHNS 180
Qy 106 LLALEPGILDTANVEALRLAGLQQLDEGLFSLRLNLDHLDVSDNOLRVPVIRGLRG 165
Db 181 LLALEPGILDTANVEALRLAGLQQLDEGLFSLRLNLDHLDVSDNOLRVPVIRGLRG 240
Qy 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGSLGFLPRLRLLLAAARNPF 225
Db 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGSLGFLPRLRLLLAAARNPF 300
Qy 226 NCVCPLSWFGFWRESHVITLASPEETRCHFPKKNAGRLILLELDYADGCCPATTTATVPT 285
Db 301 NCVCPLSWFGFWRESHVITLASPEETRCHFPKKNAGRLILLELDYADGCCPATTTATVPT 360
Qy 286 TRPVVREPTALSSSLAPTMLSPATAPATEAPSPSTAPPTVGPVPOQDCCPSTCLNGTC 345
Db 361 TRPVVREPTALSSSLAPTMLSPATAPATEAPSPSTAPPTVGPVPOQDCCPSTCLNGTC 420
Qy 346 HLGTRHHLACLCPGEGFTGLYCESQMGQTRPPTVTPRPPRSRLTLGIEPVSVTSRLVGL 405

Db	421	HLGTRHLCACLEPGFTGLYCSQMGOGTRPSFTPVTPRPRLSLTIGEPVSPTRSLRVLG	480	PRIOR FILING DATE: 1998-05-28
Qy	406	QRYLQSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLBYTTLQRLPNATYSCVWPLGP	465	PRIOR FILING DATE: 1998-06-02
Db	481	QRYLQSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLBYTTLQRLPNATYSCVWPLGP	540	PRIOR FILING DATE: 1998-06-02
Qy	466	GRYPEGEACEGAEHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR	525	PRIOR FILING DATE: 1998-06-02
Db	541	GRYPEGEACEGAEHTPPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVR	600	PRIOR FILING DATE: 1998-06-02
Qy	526	RGMAAAAADKQVFGAGPGLLEGVKVPLBPGPKATGGGEALPGSGSECEVPLMGPPG	585	PRIOR FILING DATE: 1998-06-04
Db	601	RGMAAAAADKQVFGAGPGLLEGVKVPLBPGPKATGGGEALPGSGSECEVPLMGPPG	660	PRIOR FILING DATE: 1998-06-04
Qy	586	PGLOSPPLHAKPYI	598	PRIOR FILING DATE: 1998-06-04
Db	661	PGLOSPPLHAKPYI	673	PRIOR FILING DATE: 1998-06-04
RESULT 10				
US-09-992-598-52				
; Sequence 52, Application US/09992598				
; Patent No. 6956108				
; GENERAL INFORMATION:				
; APPLICANT: Ashkenazi, Avi J.				
; APPLICANT: Baker, Kevin P.				
; APPLICANT: Botstein, David				
; APPLICANT: Desnoyers, Luc				
; APPLICANT: Eaton, Dan L.				
; APPLICANT: Ferrara, Napoleone				
; APPLICANT: Fong, Sherman				
; APPLICANT: Gerber, Hanspeter				
; APPLICANT: Gerritsen, Mary E.				
; APPLICANT: Goddard, Audrey				
; APPLICANT: Godowski, Paul J.				
; APPLICANT: Grimaldi, J. Christopher				
; APPLICANT: Gurney, Austin L.				
; APPLICANT: Kljavin, Ivar J.				
; APPLICANT: Napier, Mary A.				
; APPLICANT: Pan, James				
; APPLICANT: Paoni, Nicholas F.				
; APPLICANT: Roy, Margaret Ann				
; APPLICANT: Stewart, Timothy A.				
; APPLICANT: Tumas, Daniel				
; APPLICANT: Watanabe, Colin K.				
; APPLICANT: Williams, P. Mickey				
; APPLICANT: Wood, William I.				
; APPLICANT: Zhang, Zemin				
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				
; FILE REFERENCE: P2730PIC20				
; CURRENT APPLICATION NUMBER: US/09/992,598				
; CURRENT FILING DATE: 2001-11-14				
; PRIOR APPLICATION NUMBER: 60/049787				
; PRIOR FILING DATE: 1997-06-16				
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; PRIOR APPLICATION NUMBER: 60/089801
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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 2; Length 673;
Best Local Similarity 88.7%; Pred. No. 3.8e-213;
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

Qy 1 MCSRVPLLLPLLLALLGPGVQGCPCSCQSQPOTVFCRTARQGTTPRDRVPPDTVGLVVF 60
Db 1 MCSRVPLLLPLLLALLGPGVQGCPCSCQSQPOTVFCRTARQGTTPRDRVPPDTVGLVVF 60

Qy 61 ENGITMLDASSFAGLPGQLDLSONQIAS----- 90
Db 61 ENGITMLDAGSFAGLPGQLDLSONQIASLPSGVFQPLANLSNLDLTANRLHEITNETFF 120

Qy 91 ----- 105
Db 121 RGLRRLRLYLGKNRIRHIQGAFTDLRLLEKLQNELRALPPLRLPRLLLDLSHNS 180

Qy 106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSLRLNLDLDVSDNOLERVPPVIRGLRG 165
Db 181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSLRLNLDLDVSDNOLERVPPVIRGLRG 240

Qy 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGLSLPRLRLAAARNPF 225
Db 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGLSLPRLRLAAARNPF 300

Qy 226 NCVCPLSWFGPWVRESHVTLASPEETRCHPPKKNAGRLLLLELDYADFGCPATTTATVPT 285
Db 301 NCVCPLSWFGPWVRESHVTLASPEETRCHPPKKNAGRLLLLELDYADFGCPATTTATVPT 360

Qy 286 TRPVVREPTALSSSLAPTWSPTAPATEAPSPSTAPTVPQPODCCPSTCLNGGTC 345
Db 361 TRPVVREPTALSSSLAPTWSPTAPATEAPSPSTAPTVPQPODCCPSTCLNGGTC 420

Qy 346 HLGTRHHLACLCPGFTGLYCESQMGQTRPSPTVTPRPRSITLTIETVPSLSRVLG 405
Db 421 HLGTRHHLACLCPGFTGLYCESQMGQTRPSPTVTPRPRSITLTIETVPSLSRVLG 480

Qy 406 QRYLQSSVOLRSRLTYRNLSGPDKELVTLRLPASLAETVTLRNNATYSVCVMPILGP 465
Db 481 QRYLQSSVOLRSRLTYRNLSGPDKELVTLRLPASLAETVTLRNNATYSVCVMPILGP 540

Qy 466 GRVPEGEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
Db 541 GRVPEGEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 600

Qy 526 RGRAMAAAAQDKQVGPAGPBLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP 585
Db 601 RGRAMAAAAQDKQVGPAGPBLEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP 660

Qy 586 PGLQSPHAKPYI 598
Db 661 PGLQSPHAKPYI 673

RESULT 11
US-09-520-781-10
; Sequence 10, Application US/09520781
; Patent No. 6689866
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 653

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-187-10

Query Match      10.7%; Score 337; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

QY 7 LLLPLLLL-----LALGPGVQGCSPGSCCS-QPQTVCTARQGTTPVRDVPD 53
Db 17 ILLPFVYLTAQVWLCAIAAASAGPQNCPSVCSNQSKVCTRRGLSEVPQGISN 76
QY 54 TVGLYVFENGITMLDASSFAGLPGQLLDLSQNOIASLR-----LPELLLLDLSHNSLL 107
Db 77 TRYLMENNIIQMIQADTFRHLHLEVLQGRNSIRQIEVGAENGLASLSTLELFDNWL 136
QY 108 ALEPGILDAN-----VEALRLAGLG-----LQQLDEGLFSRLR 141
Db 137 VIPSGAFYLSKRLRLWLNPNPIESIPSYAFNRVPSLMRLDLGELKKLEYISEGAFGLF 196
QY 142 N-----LHLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIA 178
Db 197 NLKYLNLGMCNIKMPNLTPLVGLLEEMSGNHFPETRPGSFHGLSLKLLWM-NSQVS 255
QY 179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLRPLRLALAA---RNPENCVCPLSWFG 235
Db 256 LIERNAFDGLASLVELNLAHNLSLPHD---LFTPLRLYLVELHLHHPNWCDCDILWLA 312
QY 236 PWRESHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
Db 313 WWLRE-YIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSA-----PFIMDAPRLNI 364
QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTVGPVQP-----QDCPPSTC 339
Db 365 SEGRMAELKCRTPPMSSVKVLLPNGTVLASHASRHPRIISVLNDGTLNFSHVLLSDTVYTC 424
QY 340 -----LNGTCHLGRHLACLCPGFTGLYCESOMQGTTRSPPTVP- 383
Db 425 MGTNVAGNSASAYLNGSTAEALNTSNY-----SFFTGTGETTEISPDTRTKY 473
QY 384 RPPRSLLTGLIEPVSPTSRLVGLQRYLOGSSVQLRSLRLTYRNLSPDKRLVTLRLPASLA 443
Db 474 KPVPTTSGYQPAYTSTTVLIQ-----TTTRVPKQVA 505
QY 444 EYTVTLQRPNATYSVCVMPLGGRVPEGBEACGEAHTPPAVHNSHAPVTOAREGNLPLLI 503
Db 506 -----VPATD-----TTDKMQTSLDEVMTTK-----II 529
QY 504 APALAAVLLAALAAVGAAYCVRR---GRAMAAAAQDKGVGPGAGLEGVKVPLEBGP 560
Db 530 IGCFAVATLLAAMLIIVFYKLRKRHQORSTVTAAR-----TVEIIQVD-EDIP 576
QY 561 KATEGGGEALPSG 573
Db 577 AATSAATAAPSG 589

RESULT 13
US-09-957-187-10
; Sequence 10, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
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; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-187-10

Query Match      10.7%; Score 337; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

QY 7 LLLPLLLL-----LALGPGVQGCSPGSCCS-QPQTVCTARQGTTPVRDVPD 53
Db 17 ILLPFVYLTAQVWLCAIAAASAGPQNCPSVCSNQSKVCTRRGLSEVPQGISN 76
QY 54 TVGLYVFENGITMLDASSFAGLPGQLLDLSQNOIASLR-----LPELLLLDLSHNSLL 107
Db 77 TRYLMENNIIQMIQADTFRHLHLEVLQGRNSIRQIEVGAENGLASLSTLELFDNWL 136
QY 108 ALEPGILDAN-----VEALRLAGLG-----LQQLDEGLFSRLR 141
Db 137 VIPSGAFYLSKRLRLWLNPNPIESIPSYAFNRVPSLMRLDLGELKKLEYISEGAFGLF 196
QY 142 N-----LHLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIA 178
Db 197 NLKYLNLGMCNIKMPNLTPLVGLLEEMSGNHFPETRPGSFHGLSLKLLWM-NSQVS 255
QY 179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLRPLRLALAA---RNPENCVCPLSWFG 235
Db 256 LIERNAFDGLASLVELNLAHNLSLPHD---LFTPLRLYLVELHLHHPNWCDCDILWLA 312
QY 236 PWRESHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTA 295
Db 313 WWLRE-YIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSA-----PFIMDAPRLNI 364
QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTVGPVQP-----QDCPPSTC 339
Db 365 SEGRMAELKCRTPPMSSVKVLLPNGTVLASHASRHPRIISVLNDGTLNFSHVLLSDTVYTC 424
QY 340 -----LNGTCHLGRHLACLCPGFTGLYCESOMQGTTRSPPTVP- 383
Db 425 MGTNVAGNSASAYLNGSTAEALNTSNY-----SFFTGTGETTEISPDTRTKY 473
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Db 474 KPVPTTSGYQPAYTSTTVLIQ-----TTTRVPKQVA 505
QY 444 EYTVTLQRPNATYSVCVMPLGGRVPEGBEACGEAHTPPAVHNSHAPVTOAREGNLPLLI 503
Db 506 -----VPATD-----TTDKMQTSLDEVMTTK-----II 529
QY 504 APALAAVLLAALAAVGAAYCVRR---GRAMAAAAQDKGVGPGAGLEGVKVPLEBGP 560
Db 530 IGCFAVATLLAAMLIIVFYKLRKRHQORSTVTAAR-----TVEIIQVD-EDIP 576
QY 561 KATEGGGEALPSG 573
Db 577 AATSAATAAPSG 589

RESULT 13
US-09-957-187-10
; Sequence 10, Application US/09957187
; Patent No. 6942992
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
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; TITLE OF INVENTION: MEGP-, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 15966-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/520,781
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-991-053-10

Query Match 10.7%; Score 337; DB 2; Length 653;
Best Local Similarity 23.6%; Pred. No. 5.1e-16;
Matches 159; Conservative 77; Mismatches 231; Indels 206; Gaps 25;

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Db 77 TRYLMENNIIQIADTFRHLHLEVLQLGNSIRQIEVGAFNGLASLSTLELFDNWL 136
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QY 108 ALEPGILDAN-----VEALRLAGLG-----LQQLDEGLFSRLR 141
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Db 137 VIPSGAFYLSKLRELWLRNNPIESIPYAFNRVPSLMDLGLKLEYISEGAFGLF 196
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QY 142 N-----LHLDLVDSDNQLERV-PPVIRGLGLTRLRLAGNTRIA 178
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Db 197 NLKYLNLGMCNIKOMPNTPLVLGLEELEMNGHPEIRPGSFHGLSSLKLLWM-NSQVS 255
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QY 179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAA---RNPFCVCPLSWFG 235
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Db 256 LIERNAFDGLASLVELNLAHNLSLPHD---LFTPLRYLVELHLHNPWNCDCDILWLA 312
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Db 313 WMLRE-YIPTNSTCCGRCHAPMHRGRYLVVDQASFCSCA-----PFTMDAPRDLNI 364
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QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPPTAPPTVGPVQP-----QDCPSTC 339
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QY 340 -----LNGTCHLGRHHLACLCPGFTGLYCESQMGQTRPSPTVTP-- 383
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Db 425 MGTNVAGNSNAYLNGSTAEINTSNY-----SFTTGTGETTISPEDTTRKY 473
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QY 384 RPPRSLTGLIEPVSPTSLRVGLQRYLQSSVQLRSLRLTYRNLSPGKRLVTLRLPASLA 443
   ||| : |
Db 474 KPVTSTGYQPAYTTSTTVLIQ-----TTRVPKQVA 505
   ||| : |
QY 444 EYTVTLRPNATYSCVMPLGPGRVPEGEACGEAHTPPAVHSNHPVTOAREGNLPLLI 503
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Db 506 -----VPATD-----TTDKMQTSLDEVMTTK-----II 529
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QY 504 APALAAVLLAALAAVGAAYCYRR---GRAMAAAAQDKGQVGPAGLSEGVKVPLEPGP 560
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Db 530 IGCFAVTLAAAMLIVFYKLKRHQQRSTVTAAR-----TVELIQVD-EDIP 576
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QY 561 KATEGGEALPSG 573
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Db 577 AATSAATAAPSG 589
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RESULT 14

US-09-520-781-12
; Sequence 12, Application US/09520781
; Patent No. 668986

; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 668986661 polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US/09/520,781
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-520-781-12

Query Match 10.6%; Score 333; DB 2; Length 590;
Best Local Similarity 25.8%; Pred. No. 8.7e-16;
Matches 130; Conservative 60; Mismatches 187; Indels 126; Gaps 18;

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QY 7 LLLPLLLL-----LALGPGVQGCPCGSCCS-QPOTVFCTARQGTTPRDVPPD 53
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Db 17 ILLPFVLTAAQWILCAIAAASAGPQNCPSVCSCNQFSKVCTRGSEVPQGPSN 76
   ||| : |
QY 54 TVGLYVFENGITMLDASSFAGLPGQLLDLSQNIASLR-----LPRLLLDLSHNSLL 107
   ||| : |
Db 77 TRYLMENNIIQIADTFRHLHLEVLQLGNSIRQIEVGAFNGLASLSTLELFDNWL 136
   ||| : |
QY 108 ALEPGILDAN-----VEALRLAGLG-----LQQLDEGLFSRLR 141
   ||| : |
Db 137 VIPSGAFYLSKLRELWLRNNPIESIPYAFNRVPSLMDLGLKLEYISEGAFGLF 196
   ||| : |
QY 142 N-----LHLDLVDSDNQLERV-PPVIRGLGLTRLRLAGNTRIA 178
   ||| : |
Db 197 NLKYLNLGMCNIKOMPNTPLVLGLEELEMNGHPEIRPGSFHGLSSLKLLWM-NSQVS 255
   ||| : |
QY 179 QLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAA---RNPFCVCPLSWFG 235
   ||| : |
Db 256 LIERNAFDGLASLVELNLAHNLSLPHD---LFTPLRYLVELHLHNPWNCDCDILWLA 312
   ||| : |
QY 236 PWVRESHVTLASPEETRCCHPPKAGRLLELDYADFCGCPATTTTATVPTTRPVVREPTA 295
   ||| : |
Db 313 WMLRE-YIPTNSTCCGRCHAPMHRGRYLVVDQASFCSCA-----PFTMDAPRDLNI 364
   ||| : |
QY 296 LSSSLAP-----TWLSPTAPA-TEAPSPPTAPPTVGPVQP-----QDCPSTC 339
   ||| : |
Db 365 SEGRMAELKCRTPPMSSVKWLLPNGTVLSHARHPRISVLDNGTLNFSHVLSDTGVTTC 424
   ||| : |
QY 340 -----LNGTCHLGRHHLACLCPGFTGLYCESQMGQTRPSPTVTP-- 383
   ||| : |
Db 425 MGTNVAGNSNAYLNGSTAEINTSNY-----SFTTGTGETTISPEDTTRKY 473
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QY 384 RPPRSLTGLIEPVSPTSLRVGLQ 406
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Db 474 KPVTSTGYQPAYTTSTTVLIQ 496
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RESULT 15

US-09-957-187-12
; Sequence 12, Application US/09957187
; Patent No. 6863889
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-187-12

Query Match 10.6%; Score 333; DB 2; Length 590;
Best Local Similarity 25.8%; Pred. No. 8.7e-16;
Matches 130; Conservative 60; Mismatches 187; Indels 126; Gaps 18;

QY	7	LLPLLL-----LALGPVGQCPSCQCS-QPQTVFCTARQGTTPRDVPPD	53
Db	17	ILLPFVYLTAQWILCAIAAASAGPQCSCSNQFSKVCTRRGLSEVPQGI	76
QY	54	TVGLYVFENGITMLDASSFAGLPGLQLLDLSONQIASLR-----LPRL	107
Db	77	TRYLNMENNIQMIQADTFRLHLEVLQLGRNSIRQIEVGAFNGLASLS	136
QY	108	ALEPGILDTAN-----VEALRLAGLG-----LQQLDEGLFSRLR	141
Db	137	VIPSGAFYLSKRLRELNRNPIESIPSYAFNRVPSLMRLDILGELKLEYI	196
QY	142	N-----LHDLVDSDNQLERV-PPVIRGLRGLRLRLAGNTRIA	178
Db	197	NKYLNLGMCNIKOMPNTPLVGLBELEMSGNHFFPIRPGSFHGLSSLK	255
QY	179	QLRPEDLAGLAALQELDVSNLSLQALPGDLGSLFPRRLRLAAA---R	235
Db	256	LIERNAFDGLASLVELNLAHNNLSLPHD---LFTPLRYLVELHLHNP	312
QY	236	PWVRESHVTLASPEETRCHFPFPKNAGRLLLELDYADFGCPATTTAT	295
Db	313	WMLRE-YIPTNSTCCGRCHAPMHMRGYLVEYDQASFOCSA-----	364
QY	296	LSSSLAP-----TWLSPTAPA-TEAPSPSTAPPTGVPVQPQ-----	339
Db	365	SEGRMAELKCRTPPMSSVKWLLPNGTVLSHARHPRI SVLNDGTLNFS	424
QY	340	-----LNGGTCHLGTTRHILACLCEGFTGLYCESOMGQGRPSPT	383
Db	425	MGTNVAGNSNASAYLNGSTAEALNTSNY-----SFFTGTGETTEI	473
QY	384	RPPRSLTGLIEPVSPISLRVGLQ	406
Db	474	KPVTTTGTGYQPAYTTTSTVLIQ	496

Search completed: January 5, 2006, 13:53:41
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 5, 2006, 13:48:58 ; Search time 19 Seconds
(without alignments)
3028.296 Million cell updates/sec

Title: US-09-943-780-69
Perfect score: 3135
Sequence: 1 MCSRVPLLLPLLLLLLALPGP.....PLMGFPGLQSLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	281.5	9.0	603	2	JC1282
5	278.5	8.9	603	2	JC6128
6	278	8.9	1531	2	T42218
7	264.5	8.4	420	2	A53531
8	261	8.3	1523	2	T13953
9	255.5	8.1	1469	2	B36685
10	255.5	8.1	1480	2	A36685
11	251	8.0	622	2	JC7973
12	243.5	7.8	312	1	NBHUIA
13	240	7.7	560	2	A60164
14	237	7.6	707	2	JC7763
15	231	7.4	1025	2	T42626
16	222.5	7.1	536	2	A34901
17	214.5	6.8	1535	2	S46224
18	212.5	6.8	361	2	A53860
19	210.5	6.7	4302	2	A38971
20	209	6.7	1091	2	A58532
21	208.5	6.7	382	2	T39088
22	200	6.4	653	2	T25194
23	199	6.3	1328	2	T23007
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25	194.5	6.2	1355	2	T28714
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28	192.5	6.1	575	2	T29972
29	189	6.0	369	2	S20811

30	189	6.0	369	2	S32793
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32	188.5	6.0	440	2	A47530
33	186	5.9	440	2	A39613
34	184	5.9	368	1	BGHUN
35	183	5.8	662	2	S42799
36	182	5.8	369	2	S32559
37	181.5	5.8	357	2	S24317
38	177.5	5.7	2493	2	A55481
39	176.5	5.6	1495	2	T31434
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41	173	5.5	925	2	JC2033
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43	172	5.5	1134	2	T04587
44	170.5	5.4	2145	2	JC4747
45	170	5.4	907	2	JE0176
46	169.5	5.4	760	2	T06291
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48	169	5.4	839	2	F75518
49	168.5	5.4	907	2	JG0193
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51	167	5.3	1112	2	T10504
52	166.5	5.3	549	2	T41744
53	166.5	5.3	800	2	AB1129
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58	165	5.3	994	2	H96510
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60	162	5.2	242	2	T14791
61	161	5.1	559	2	T42998
62	161	5.1	682	2	A49121
63	161	5.1	682	2	A43318
64	160.5	5.1	2910	2	T42214
65	160	5.1	744	2	E86255
66	159.5	5.1	1112	2	T00952
67	159	5.1	572	2	T30947
68	159	5.1	613	2	A88684
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70	159	5.1	1119	2	AD1822
71	158.5	5.1	738	2	T19938
72	158	5.0	1066	2	T15864
73	158	5.0	3570	2	T45025
74	156.5	5.0	360	2	I47020
75	156.5	5.0	980	2	H84632
76	156	5.0	354	2	S29145
77	156	5.0	594	2	T23841
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79	155.5	5.0	1334	2	T50568
80	155	4.9	961	2	T23395
81	154.5	4.9	1013	2	T10659
82	154.5	4.9	1143	2	T10636
83	154.5	4.9	1192	2	T48499
84	154.5	4.9	1495	2	S60255
85	153.5	4.9	864	2	T08575
86	153.5	4.9	894	1	A41527
87	153	4.9	699	2	C43674
88	152	4.8	786	2	T08664
89	151.5	4.8	695	1	JN0898
90	151	4.8	540	2	T12704
91	151	4.8	1389	2	T13852
92	150.5	4.8	695	1	QRHUT
93	150.5	4.8	1109	2	T18536
94	150	4.8	1134	1	A29944
95	149.5	4.8	224	2	T32185
96	149.5	4.8	696	2	JC7361
97	149	4.8	1025	1	A57676
98	149	4.8	1143	2	B84431
99	149	4.8	2357	2	A59249
100	148.5	4.7	375	2	S05390
101	148.5	4.7	610	2	T23836
102	148.5	4.7	680	2	T19939

biglycan precursor
extensin homolog F
oligodendrocyte-my
oligodendrocyte-my
biglycan precursor
garp precursor - h
biglycan precursor
decorin precursor
adenylate cyclase
densin-180 - rat
lumican precursor
G protein-coupled
decorin precursor
hypothetical prote
adenylate cyclase
orphan G protein-c
extensin homolog T
decorin precursor
hypothetical prote
G protein-coupled
internalin A precu
disease resistance
hypothetical prote
hypothetical A limpo
decorin precursor
hypothetical prote
gene flightless-I
flightless-I homol
probable disease r
extensin homolog F
hypothetical prote
Ras-binding protei
cell-surface molec
connectin precurs
otogelin - mouse
hypothetical prote
hypothetical prote
hypothetical prote
protein AC7.2 [imp
hypothetical prote
leucine-rich-repea
hypothetical prote
hypothetical prote
mucin MUC5B, trach
decorin - rabbit
probable receptor-
N-chimerin homolog
hypothetical prote
probable multi-dom
hypothetical prote
probable serine/th
hypothetical prote
receptor-like prot
transcription co-r
protein kinase hom
protein-tyrosine k
US4 protein - huma
Toll protein-like
folliculin recept
leucine-rich prote
gene wheeler prote
folliculin recept
receptor-like prot
chaotrin precursor
hypothetical prote
folliculin recept
protein kinase Xa2
probable receptor
class VII unconven
fibromodulin precu
hypothetical prote
hypothetical prote

103	148.5	4.7	890	2	C96654	hypothetical prote	176	136	4.3	4957	2	T03455	ALR protein - huma
104	148.5	4.7	964	2	T49038	hypothetical prote	177	135.5	4.3	427	2	UC4915	ags protein precu
105	148.5	4.7	1115	2	S40241	G protein-coupled	178	135.5	4.3	499	2	D83333	hypothetical prote
106	148	4.7	338	2	S52284	lumicon, secretory	179	135.5	4.3	1124	2	B84742	probable receptor-
107	148	4.7	1188	2	S49915	extensin-like prot	180	135.5	4.3	5262	2	T03454	ALR protein - huma
108	147.5	4.7	316	2	A41781	proteoglycan-Lb -	181	135	4.3	601	2	S56144	SH3 domain binding
109	147.5	4.7	1385	2	T13887	tlr protein - frui	182	134.5	4.3	613	2	T15489	hypothetical prote
110	147	4.7	1964	2	T09059	notch4 - mouse	183	134.5	4.3	847	2	F96531	hypothetical prote
111	147	4.7	2414	2	A54277	transcription adap	184	134.5	4.3	1039	2	T22117	hypothetical prote
112	146.5	4.7	382	2	T04260	hypothetical prote	185	134	4.3	530	2	A45690	transactivator EBN
113	146.5	4.7	925	2	C84538	probable LRR recep	186	134	4.3	656	2	B47096	hylB homolog - Str
114	146.5	4.7	1408	2	S16148	gene serrate prote	187	134	4.3	886	2	T40734	probable adenylate
115	146	4.7	369	2	G83434	translocation prot	188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
116	145.5	4.6	380	2	S71876	fibromodulin - chi	189	133.5	4.3	384	2	A41710	promastigote surfa
117	145.5	4.6	886	2	S29605	Glycoprotein 350/2	190	133.5	4.3	1068	2	F96769	hypothetical prote
118	145.5	4.6	2142	2	B35098	MHC class III hist	191	133	4.2	576	2	T36729	probable serine/th
119	145	4.6	458	2	T19941	hypothetical prote	192	133	4.2	852	2	S15129	tyrosine kinase C
120	145	4.6	679	2	T20713	hypothetical prote	193	133	4.2	932	2	T48489	receptor-like prot
121	145	4.6	694	2	JC2327	foliitropin recept	194	133	4.2	1257	2	A88536	protein B0523.5 [i
122	145	4.6	1839	1	OVBXK	adenylate cyclase	195	133	4.2	4391	2	A38096	perlecan precursor
123	144.5	4.6	486	2	B86460	hypothetical prote	196	132.5	4.2	463	1	A36479	milk fat globule m
124	144.5	4.6	2187	2	T30826	nascent polypeptid	197	132.5	4.2	2035	1	A40718	host cell factor C
125	144.5	4.6	3149	1	Q0BE8	BPLF1 protein - hu	198	132	4.2	3164	1	WMBEH6	UL36 protein - hum
126	144	4.6	695	2	I45896	follicle stimulati	199	131.5	4.2	346	2	T46916	hypothetical prote
127	144	4.6	1019	2	C96519	probable disease r	200	131.5	4.2	890	2	T00800	disease resistance
128	144	4.6	3020	2	A43932	mucin 2 precursor,	201	131.5	4.2	1097	2	A29943	Toll protein presu
129	143.5	4.6	243	2	B41710	promastigote surfa	202	131.5	4.2	1286	2	A88396	protein M0E10.2 [
130	143.5	4.6	476	2	T27051	hypothetical prote	203	131	4.2	612	2	T10727	protein kinase Xa2
131	143.5	4.6	496	2	C96832	hypothetical prote	204	131	4.2	767	2	B84594	probable LRR recep
132	143.5	4.6	605	2	T50817	protein serine/thr	205	131	4.2	905	2	T00475	probable disease r
133	143.5	4.6	683	2	T24486	hypothetical prote	206	131	4.2	915	2	T09575	smoothelin - human
134	142.5	4.5	1870	2	S37671	MHC class III hist	207	131	4.2	1095	2	C96746	hypothetical prote
135	142.5	4.5	1872	2	S36152	MHC class III hist	208	131	4.2	1196	2	T09356	brassinosteroid-in
136	142	4.5	661	2	S56258	RP105 - mouse	209	130.5	4.2	448	2	T27395	hypothetical prote
137	142	4.5	983	2	G84524	probable disease r	210	130	4.1	268	2	T19697	hypothetical prote
138	141.5	4.5	462	2	D84858	hypothetical prote	211	130	4.1	389	2	H86266	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote	212	130	4.1	395	2	H75457	hypothetical prote
140	141.5	4.5	1029	2	T05050	protein kinase hom	213	130	4.1	768	2	T17462	disease resistance
141	141.5	4.5	1051	2	T13174	gp150 protein - fr	214	130	4.1	800	2	H84740	hypothetical prote
142	141	4.5	630	2	AC1129	Internalin B [impo	215	129.5	4.1	315	2	T06806	proline rich prote
143	141	4.5	717	2	T33295	hypothetical prote	216	129.5	4.1	780	2	T00366	hypothetical prote
144	140.5	4.5	376	2	S55275	fibromodulin precu	217	129.5	4.1	861	2	A48825	Notch homolog Motc
145	140	4.5	277	2	I60122	rau-1 homolog - hu	218	129.5	4.1	912	2	A54423	brevian-tyrosine k
146	140	4.5	474	2	S85763	chitinase (EC 3.2.	219	129.5	4.1	942	2	S23251	protein-tyrosine k
147	140	4.5	754	2	A85043	probable LRR recep	220	129.5	4.1	1173	2	S50620	prockr2 - chicken
148	140	4.5	1029	2	T00712	protein kinase hom	221	129.5	4.1	1469	2	T09219	basal transcriptio
149	139.5	4.4	333	2	T34555	hypothetical prote	222	129	4.1	371	2	S20075	promastigote surfa
150	139.5	4.4	527	2	A75399	hypothetical prote	223	129	4.1	835	2	T05259	probable disease r
151	139.5	4.4	539	2	G70520	probable csp prote	224	129	4.1	910	2	B96770	hypothetical prote
152	139.5	4.4	4351	2	T00252	MEGF1 protein - ra	225	129	4.1	1027	2	B85089	receptor protein k
153	139	4.4	581	2	A45551	insect-stage-speci	226	129	4.1	1064	2	B86465	probable Protein k
154	139	4.4	603	2	T24315	hypothetical prote	227	129	4.1	1232	2	T05322	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote	228	129	4.1	1329	2	A64828	cell division prot
156	139	4.4	1088	2	E86312	FilA6.9 protein -	229	129	4.1	1342	2	E85614	cell division prot
157	139	4.4	2240	2	T37057	probable multi-dom	230	129	4.1	1342	2	G90750	cell division prot
158	138.5	4.4	342	2	A46743	lumican precursor	231	129	4.1	1959	1	AGRT	agrin - rat
159	138.5	4.4	990	2	T14756	hypothetical prote	232	129	4.1	2321	1	S78549	notch3 protein - h
160	138.5	4.4	1650	2	S53457	dominant autoantig	233	128.5	4.1	487	2	S42442	nuclear protein EB
161	138	4.4	630	2	C39930	hypothetical prote	234	128.5	4.1	677	2	H86208	protein F22G5.26 [
162	138	4.4	858	2	T00258	hypothetical prote	235	128.5	4.1	727	2	C84534	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote	236	128.5	4.1	744	2	C84527	probable receptor-
164	137.5	4.4	1151	2	T18535	high molecular mas	237	128.5	4.1	825	2	T29634	hypothetical prote
165	137.5	4.4	4660	2	T42737	gp330 protein prec	238	128.5	4.1	1113	2	T00271	hypothetical prote
166	137	4.4	562	2	T34319	hypothetical prote	239	128.5	4.1	3968	2	A44265	trithorax homolog
167	137	4.4	695	2	JC1493	foliitropin recept	240	128	4.1	597	2	S72468	probable transcrip
168	137	4.4	788	2	AG0786	secreted effector	241	128	4.1	967	2	T48210	hypothetical prote
169	137	4.4	907	1	Q0BE21	membrane antigen g	242	128	4.1	1428	2	T08852	lustrin A - Califo
170	137	4.4	4544	1	S23292	alpha-2-macroglobu	243	128	4.1	1914	2	T42635	tenascin Y precurs
171	137	4.4	4545	1	S25111	alpha-2-macroglobu	244	127.5	4.1	750	2	D86245	hypothetical prote
172	136	4.3	322	2	S72271	proteoglycan lb pr	245	127.5	4.1	1120	2	B86479	hypothetical prote
173	136	4.3	626	2	A80123	probable antigenic	246	127.5	4.1	1784	2	C96615	hypothetical prote
174	136	4.3	692	2	A34548	foliitropin recept	247	127	4.1	327	2	S20074	promastigote surfa
175	136	4.3	1008	2	D84434	probable receptor-	248	127	4.1	773	2	T00502	probable receptor-

249 127 4.1 775 1 EDBE11 immediate-early pr
 250 127 4.1 800 2 G84740 hypothetical prote
 251 127 4.1 1366 2 T35985 probable large pro
 252 127 4.1 1895 2 T06609 disease resistance
 253 127 4.1 1955 1 AGCH agrin precursor -
 254 126.5 4.0 268 2 T45616 hypothetical prote
 255 126.5 4.0 685 2 JC7570 Delta-4 protein -
 256 126.5 4.0 694 2 T46301 follitropin recept
 257 126.5 4.0 862 2 T46289 hypothetical prote
 258 126.5 4.0 999 1 S27566 receptor-like prot
 259 126.5 4.0 1091 2 T33596 protein-tyrosine k
 260 126.5 4.0 1777 2 T34369 hypothetical prote
 261 126 4.0 500 2 S49302 AWL218 protein -
 262 126 4.0 865 2 A47282 calcium-binding pr
 263 126 4.0 873 2 A47283 calphotin - fruit
 264 126 4.0 996 2 F96410 protein F3M18.12
 265 126 4.0 1152 2 T31911 hypothetical prote
 266 126 4.0 1820 2 A55494 latent transformin
 267 125.5 4.0 283 2 S13383 hydroxyproline-ric
 268 125.5 4.0 548 2 AH1107 internalin H [impo
 269 125.5 4.0 635 2 F75477 hypothetical prote
 270 125.5 4.0 764 2 A40077 thyrotropin recept
 271 125.5 4.0 1003 2 T05898 hypothetical prote
 272 125 4.0 350 2 S22456 hydroxyproline-ric
 273 125 4.0 476 2 A36478 surface glycoprote
 274 125 4.0 783 2 T45899 receptor protein k
 275 125 4.0 818 2 F96586 hypothetical prote
 276 125 4.0 991 2 T52400 receptor-like prot
 277 125 4.0 1504 2 T49896 glycine/proline-ri
 278 125 4.0 2026 1 ORBY adenylyate cyclase
 279 124.5 4.0 298 2 B35272 oteoinductive fac
 280 124.5 4.0 756 2 T27642 hypothetical prote
 281 124.5 4.0 849 2 C97303 hypothetical prote
 282 124.5 4.0 910 2 G84648 probable disease r
 283 124.5 4.0 977 2 C96745 hypothetical prote
 284 124.5 4.0 1223 2 E88451 protein K10D2.1 [i
 285 124.5 4.0 2176 2 T13806 toucan gene protei
 286 124 4.0 496 2 D75261 conserved hypotet
 287 124 4.0 543 2 S35047 mucin JUL7 - human
 288 124 4.0 574 2 T43556 Wiskott-Aldrich sy
 289 124 4.0 605 2 AG0123 probable antigenic
 290 124 4.0 729 2 E70803 hypothetical prote
 291 124 4.0 766 2 B95440 receptor kinase-1i
 292 124 4.0 978 2 E86787 protein T4012.5 [i
 293 124 4.0 1011 2 T45718 receptor-kinase li
 294 124 4.0 1472 2 B54772 Atp binding cassel
 295 124 4.0 4135 2 T42629 tenascin-X - bovin
 296 123.5 3.9 380 2 T01281 probable leucine-r
 297 123.5 3.9 492 2 F86263 hypothetical prote
 298 123.5 3.9 656 2 AE1479 probable cell surf
 299 123.5 3.9 690 2 T41236 probable alcohol d
 300 123 3.9 528 2 T15198 hypothetical prote
 301 123 3.9 574 2 T38819 wiskott-aldrich sy
 302 123 3.9 888 2 S23065 ufo protein - mous
 303 123 3.9 1072 2 A37127 microtubule-associ
 304 123 3.9 2591 2 T30288 cristinamycin I sy
 305 122.5 3.9 303 2 S28264 hydroxyproline-ric
 306 122.5 3.9 415 2 T13435 hypothetical prote
 307 122.5 3.9 592 2 D70863 hypothetical prote
 308 122.5 3.9 699 2 T05225 extensin homolog F
 309 122.5 3.9 809 2 B84634 probable receptor-
 310 122.5 3.9 845 2 T12537 hypothetical prote
 311 122.5 3.9 1016 2 T30553 disease resistance
 312 122.5 3.9 2944 2 A54849 collagen alpha 1(V
 313 122 3.9 298 2 JC4130 osteoglycin precur
 314 122 3.9 326 2 T24722 hypothetical prote
 315 122 3.9 596 2 AE1515 internalin like pr
 316 122 3.9 623 2 T19876 hypothetical prote
 317 122 3.9 672 2 B84782 probable receptor-
 318 122 3.9 715 2 G86239 protein F20B24.6 [i
 319 122 3.9 719 2 T47727 hypothetical prote
 320 122 3.9 921 2 B86234 hypothetical prote
 321 122 3.9 992 2 T05335 hypothetical prote

322 121.5 3.9 432 2 E96712 unknown protein, 6
 323 121.5 3.9 519 2 T07026 ethylene receptor
 324 121.5 3.9 635 2 T07794 ethylene receptor
 325 121.5 3.9 686 2 JC7569 Delta-4 protein -
 326 121.5 3.9 760 2 F86387 Probable Pto Kinase
 327 121.5 3.9 902 2 T00588 hypothetical prote
 328 121.5 3.9 1251 2 A57293 latent transformin
 329 121.5 3.9 1409 2 T37188 presynaptic activi
 330 121.5 3.9 2265 1 FNBO fibronectin - bovi
 331 121.5 3.9 2297 2 T34918 polyketide synthas
 332 121.5 3.9 2318 2 S45306 notch 3 protein -
 333 121.5 3.9 3530 2 S45306 unconventional myo
 334 121 3.9 306 2 T52340 cell wall-plasma m
 335 121 3.9 480 2 T00971 sulfated disease r
 336 121 3.9 485 2 A33647 microtubule-associ
 337 121 3.9 733 2 A45301 Microtubule-associ
 338 121 3.9 1203 2 A49175 Notch B protein -
 339 121 3.9 1520 2 T00273 hypothetical prote
 340 121 3.9 2531 2 S18188 notch protein homo
 341 120.5 3.8 299 2 A35272 oteoinductive fac
 342 120.5 3.8 753 2 JQ0532 OP protein - Kenne
 343 120.5 3.8 821 2 AB1126 internalin, peptid
 344 120.5 3.8 855 2 T17460 disease resistance
 345 120.5 3.8 976 2 B84659 probable receptor-
 346 120.5 3.8 976 2 T05897 protein kinase hom
 347 120.5 3.8 981 2 T50851 receptor protein k
 348 120.5 3.8 987 2 T50850 receptor protein k
 349 120.5 3.8 1118 2 A48292 mucin, tracheobron
 350 120.5 3.8 1152 2 A33483 microtubule-associ
 351 120.5 3.8 1722 2 E89753 protein Fl1C7.4 [i
 352 120.5 3.8 1778 2 AF1116 internalin protein
 353 120.5 3.8 3566 1 A40701 tenascin-X precurs
 354 120 3.8 361 2 AH1469 internalin protein
 355 120 3.8 376 2 S71558 probable cell wall
 356 120 3.8 458 2 T31631 hypothetical prote
 357 120 3.8 892 2 T09071 SH3 domains-contai
 358 120 3.8 962 2 T04124 receptor-like prot
 359 120 3.8 1126 2 T20801 hypothetical prote
 360 120 3.8 1224 2 T40765 web1 protein homol
 361 119.5 3.8 267 2 S08314 cell wall glycopro
 362 119.5 3.8 479 1 A31753 transcription fact
 363 119.5 3.8 660 2 T45569 receptor protein k
 364 119.5 3.8 1048 1 XPBEA9 large structural p
 365 119.5 3.8 1079 2 C96772 probable receptor
 366 119.5 3.8 1166 2 F96598 protein F20N2.4 [i
 367 119.5 3.8 1400 2 B70963 hypothetical prote
 368 119.5 3.8 1596 2 A35927 190K DNA-binding p
 369 119.5 3.8 1643 2 T14274 versican precursor
 370 119 3.8 164 2 T53641 mucin 5AC - human
 371 119 3.8 352 2 S49299 AWJL172 protein -
 372 119 3.8 424 2 S27783 hypothetical prote
 373 119 3.8 550 2 C75557 hypothetical prote
 374 119 3.8 651 2 T42844 hypothetical prote
 375 119 3.8 660 1 QQBE3 BHLFI protein - hu
 376 119 3.8 808 2 T23129 hypothetical prote
 377 119 3.8 864 2 D84740 hypothetical prote
 378 119 3.8 1006 2 T42731 atrophin-1 related
 379 119 3.8 1045 2 T41119 internalin- relate
 380 118.5 3.8 222 2 H96711 hypothetical prote
 381 118.5 3.8 400 1 A39822 leukosialin precu
 382 118.5 3.8 677 2 E70722 hypothetical prote
 383 118.5 3.8 751 2 AC2098 hypothetical prote
 384 118.5 3.8 869 2 A71400 probable disease r
 385 118.5 3.8 883 2 S57653 brevicin precursor
 386 118.5 3.8 988 2 T45717 receptor-kinase 1i
 387 118.5 3.8 1173 2 T25893 hypothetical prote
 388 118.5 3.8 1356 2 A45445 Januskin precursor,
 389 118.5 3.8 1607 2 T02837 long chain fatty a
 390 118 3.8 294 2 A37232 mucin, tracheal (A
 391 118 3.8 599 2 T10798 pterophorin-S - Vo
 392 118 3.8 667 2 S74254 homeotic protein s
 393 118 3.8 823 2 AD1935 general secretion
 394 118 3.8 1134 1 JN0711 protein-tyrosine k

395	118	3.8	2471	2	A49128	cell-fate determin	468	114	3.6	378	2	S00842	leukosialin precu
396	117.5	3.7	473	2	D85041	hypothetical prote	469	114	3.6	413	1	A34888	transcription fact
397	117.5	3.7	624	2	A55576	collagen alpha 2(X	470	114	3.6	555	1	S20100	mullerian inhibiti
398	117.5	3.7	660	2	JW0067	chitinase (EC 3.2.	471	114	3.6	586	2	T29695	hypothetical prote
399	117.5	3.7	996	2	T10725	protein kinase Xa2	472	114	3.6	633	2	S62057	proline-rich prote
400	117.5	3.7	1075	2	D70568	hypothetical prote	473	114	3.6	634	2	T00388	hypothetical prote
401	117.5	3.7	1706	2	I84499	zinc finger protei	474	114	3.6	656	2	E75468	hypothetical prote
402	117	3.7	431	2	T27904	hypothetical prote	475	114	3.6	768	2	A42755	p-selectin precurs
403	117	3.7	655	1	A46688	hepatocyte growth	476	114	3.6	1290	2	T00018	period protein hom
404	117	3.7	670	2	H96707	probable receptor	477	114	3.6	2225	2	T26063	hypothetical prote
405	117	3.7	678	2	JC4245	transcription fact	478	113.5	3.6	317	2	S55316	hypothetical prote
406	117	3.7	743	2	C94633	probable disease r	479	113.5	3.6	330	2	T46256	brevican - human (
407	117	3.7	801	2	T29018	hypothetical prote	480	113.5	3.6	538	2	T01102	disease resistance
408	117	3.7	1007	2	C84668	probable receptor-	481	113.5	3.6	896	2	E43817	transforming prote
409	117	3.7	1009	2	D75399	probable penicilli	482	113.5	3.6	907	2	A86460	99.9K hypothetical
410	117	3.7	1328	2	T43060	agrin - electric r	483	113.5	3.6	938	1	Q0BE24	nuclear antigen EB
411	117	3.7	1450	2	T30273	hypothetical prote	484	113.5	3.6	1286	2	T33476	hypothetical prote
412	117	3.7	1574	2	T13954	MEGF6 protein - ra	485	113.5	3.6	1907	2	S50893	protein-tyrosine-p
413	117	3.7	2082	2	T37056	probable multi-dom	486	113.5	3.6	2911	2	T20566	hypothetical prote
414	117	3.7	2232	2	T34434	hypothetical prote	487	113	3.6	371	2	T49908	hypothetical prote
415	116.5	3.7	279	2	S53363	mucin 5AC (clone J	488	113	3.6	377	2	A48018	mucin 7 precursor,
416	116.5	3.7	439	2	S51939	chitinase (EC 3.2.	489	113	3.6	382	2	E84527	hypothetical prote
417	116.5	3.7	621	2	I38467	low density lipopr	490	113	3.6	419	2	A90888	hypothetical prote
418	116.5	3.7	787	2	T27632	hypothetical prote	491	113	3.6	419	2	H85729	hypothetical prote
419	116.5	3.7	794	2	T27633	hypothetical prote	492	113	3.6	603	2	A75373	probable N-acetyl
420	116.5	3.7	828	2	A88860	protein 2C518.3 [1	493	113	3.6	979	2	A35913	regulatory factor
421	116.5	3.7	1048	2	T31425	C-terminal domain-	494	113	3.6	982	2	A53253	microtubule-associ
422	116.5	3.7	1446	1	A45344	immediate-early pr	495	113	3.6	1002	2	T46033	receptor protein k
423	116.5	3.7	2229	2	T16199	hypothetical prote	496	113	3.6	1025	2	T45647	receptor protein k
424	116	3.7	292	2	S24169	mucin - rat	497	113	3.6	1069	2	S27922	nuclear antigen EB
425	116	3.7	652	2	S71753	repellent protein	498	113	3.6	1247	2	T42209	neural plakophilin
426	116	3.7	660	2	A23348	hypothetical prote	499	113	3.6	1343	2	AF0611	cell division prot
427	116	3.7	729	2	F86308	Similar to disease	500	113	3.6	2688	2	T49477	alpha-A-crystallin
428	116	3.7	771	2	T02565	disease resistance	501	113	3.6	3381	2	T42389	versican precursor
429	116	3.7	808	2	B97303	hypothetical prote	502	112.5	3.6	347	2	S10571	mucin 1 precursor,
430	116	3.7	845	2	T07039	Hcr-0 protein - t	503	112.5	3.6	581	2	G96811	unknown protein T1
431	116	3.7	907	2	A24938	hypothetical T2 pr	504	112.5	3.6	731	2	B86369	hypothetical prote
432	116	3.7	1291	2	T00019	period protein hom	505	112.5	3.6	1075	2	A57377	transcription fact
433	116	3.7	1494	2	T14355	protein-tyrosine-p	506	112.5	3.6	1237	2	AC1583	internalin protein
434	116	3.7	1840	2	T30250	Gri protein - mous	507	112.5	3.6	1680	2	T01367	hypothetical prote
435	116	3.7	2531	2	A46019	notch-1 protein - h	508	112.5	3.6	2479	2	F87386	conserved hypothet
436	116	3.7	2555	2	A40043	notch protein homo	509	112.5	3.6	4006	2	T09070	probable tenascin
437	116	3.7	2774	2	A43359	microtubule-associ	510	112	3.6	241	2	S32359	glial growth facto
438	115.5	3.7	322	2	A33715	apomucin precursor	511	112	3.6	252	2	T01787	thyrotropin recept
439	115.5	3.7	513	2	AC3061	hypothetical prote	512	112	3.6	253	1	JC1319	thyrotropin recept
440	115.5	3.7	513	2	D98225	hypothetical prote	513	112	3.6	285	2	A41826	probable pheromone
441	115.5	3.7	528	2	I47141	gastric mucin (clo	514	112	3.6	383	2	S53716	delta-like homeoti
442	115.5	3.7	696	2	T42659	hypothetical prote	515	112	3.6	413	2	S48756	transcription fact
443	115.5	3.7	805	2	T49385	hypothetical prote	516	112	3.6	704	2	AE2107	serine/threonine k
444	115.5	3.7	946	2	S27921	nuclear antigen EB	517	112	3.6	731	2	T04455	hypothetical prote
445	115.5	3.7	1093	2	I38533	AFI7 protein - hum	518	112	3.6	742	2	F84643	hypothetical prote
446	115.5	3.7	1268	2	S52781	neurocan - mouse	519	112	3.6	764	1	QRHURH	thyrotropin recept
447	115.5	3.7	1460	1	EDBE1F	immediate-early pr	520	112	3.6	883	2	S49126	brevican precursor
448	115.5	3.7	2214	2	T16305	hypothetical prote	521	112	3.6	960	2	G84652	probable receptor-
449	115.5	3.7	3421	1	WZBE86	367K tegument prot	522	112	3.6	990	2	T03784	probable receptor
450	115	3.7	404	2	T08549	hypothetical prote	523	112	3.6	1032	2	T34433	hypothetical prote
451	115	3.7	451	2	S74728	hypothetical prote	524	112	3.6	1289	2	AB2217	hypothetical prote
452	115	3.7	461	2	T10741	extensin-like prot	525	111.5	3.6	224	2	D72861	AcOrf-91 protein -
453	115	3.7	479	1	S22542	transcription fact	526	111.5	3.6	383	2	S32975	gene BCRF2 protein
454	115	3.7	539	2	AH1216	internalin, probab	527	111.5	3.6	478	1	I47154	transcription fact
455	115	3.7	766	2	T01817	hypothetical prote	528	111.5	3.6	645	2	T05251	probable disease r
456	115	3.7	838	2	T08423	Axin homolog Axil	529	111.5	3.6	649	2	T46500	hypothetical prote
457	115	3.7	980	2	T05414	protein kinase hom	530	111.5	3.6	1047	2	A55617	masquerade precurs
458	115	3.7	1133	2	E86308	hypothetical prote	531	111.5	3.6	1253	2	T45787	disease resistance
459	115	3.7	1220	2	A56136	jagged protein pre	532	111.5	3.6	1298	1	EDBE75	immediate-early pr
460	115	3.7	2415	1	A39086	aggreacan precursor	533	111.5	3.6	1353	1	JH0675	restrictin precurs
461	114.5	3.7	328	2	J00985	hydroxyproline-ric	534	111.5	3.6	2649	2	TS1023	hypothetical prote
462	114.5	3.7	409	2	T11743	pp47 protein - pig	535	111	3.5	274	2	JC8063	heart-restricted l
463	114.5	3.7	505	2	AC1469	internalin like pr	536	111	3.5	478	2	H86459	hypothetical prote
464	114.5	3.7	606	2	T51880	hypothetical prote	537	111	3.5	509	2	T05260	probable disease r
465	114.5	3.7	627	2	T27123	hypothetical prote	538	111	3.5	518	2	S50465	PAC2 protein - yea
466	114.5	3.7	638	2	T05606	protein kinase hom	539	111	3.5	548	2	E70546	hypothetical prote
467	114	3.6	218	2	T01104	disease resistance	540	111	3.5	603	2	S28941	coagulation factor

541 111 3.5 610 2 S35049 mucin JER57 - huma
542 111 3.5 620 2 T50150 yeast nrld1-like pr
543 111 3.5 699 1 QRHUUT lutropin-choriogon
544 111 3.5 853 2 T17461 disease resistance
545 111 3.5 932 2 T21338 hypothetrical prote
546 111 3.5 984 2 T48216 hypothetrical prote
547 111 3.5 1721 1 I38902 retinoblastoma bin
548 111 3.5 2524 2 A35844 kotch protein - Af
549 110.5 3.5 359 2 C55066 tyrosine decarboxy
550 110.5 3.5 421 2 A60058 neural cell adhesi
551 110.5 3.5 512 2 G86459 Hypothetical 55.6
552 110.5 3.5 525 1 A58674 neurotrophin-3 rec
553 110.5 3.5 533 2 T07970 aromatic-L-amino-a
554 110.5 3.5 565 2 J50338 Frizzled-2 protein
555 110.5 3.5 684 2 T01267 leucine-rich repea
556 110.5 3.5 803 1 S35695 neurotrophin-3 rec
557 110.5 3.5 815 2 B56708 extracellular sign
558 110.5 3.5 855 2 T07015 Cf-4A protein - to
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561 110.5 3.5 1207 2 T00378 KIAA0641 protein -
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563 110.5 3.5 1344 2 T14316 rig-1 protein - mo
564 110.5 3.5 1346 2 T17412 polyketide synthas
565 110.5 3.5 2476 2 T34022 hypothetrical prote
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567 110 3.5 391 2 T04609 hypothetrical prote
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569 110 3.5 691 2 D84889 probable receptor-
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577 110 3.5 1483 2 B86143 FGF3.12 protein -
578 110 3.5 1711 1 A55148 protein-tyrosine-p
579 110 3.5 2703 1 A24420 notch protein - fr
580 110 3.5 2715 2 T13049 eyelid - fruit fly
581 110 3.5 3942 2 T42730 Bassoon protein -
582 110 3.5 213 2 A86228 hypothetrical prote
583 109.5 3.5 279 2 T10361 hypothetrical prote
584 109.5 3.5 318 2 T29479 hypothetrical prote
585 109.5 3.5 428 2 B71415 probable coll wall
586 109.5 3.5 473 2 S36533 L2 protein - huma
587 109.5 3.5 507 2 T44768 antifreeze glycope
588 109.5 3.5 538 2 S57459 hook-containing pr
589 109.5 3.5 558 2 JC5878 plasma hyaluronan-
590 109.5 3.5 583 1 S22544 transcription fact
591 109.5 3.5 612 2 I73633 gene trkC protein
592 109.5 3.5 825 2 A55178 neurotrophin recep
593 109.5 3.5 839 1 I73632 neurotrophin-3 rec
594 109.5 3.5 874 2 E97302 hypothetrical prote
595 109.5 3.5 878 2 T21621 hypothetrical prote
596 109.5 3.5 954 2 T19765 hypothetrical prote
597 109.5 3.5 1299 2 T47182 hypothetrical prote
598 109.5 3.5 1776 1 RWPWTM genome polyprotein
599 109.5 3.5 2531 2 T31070 notch homolog - se
600 109.5 3.5 2717 2 A34203 DNA-binding protei
601 109.5 3.5 379 2 T05441 proline-rich prote
602 109 3.5 379 2 D85257 extensin-like prote
603 109 3.5 395 2 I52842 CD43 Lp-3 antigen
604 109 3.5 395 2 A33545 leukosialin CD43 p
605 109 3.5 403 2 S45279 prpL2 protein - hu
606 109 3.5 426 2 JQ1696 pistil extensin-li
607 109 3.5 431 2 T04868 hypothetrical prote
608 109 3.5 437 2 A54595 transcription fact
609 109 3.5 598 2 A54595 receptor-like prot
610 109 3.5 613 2 T42671 hypothetrical prote
611 109 3.5 833 2 S19087 gene Delta protein
612 109 3.5 1611 2 T38236 hypothetrical prote
613 109 3.4 1376 2 G00043

614 109 3.5 2809 2 T30213 G-cadherin - sea u
615 108.5 3.5 308 2 JC7125 epidermal growth f
616 108.5 3.5 389 2 S27200 proline-rich prote
617 108.5 3.5 402 2 A84581 probable disease r
618 108.5 3.5 418 2 T15142 hypothetrical prote
619 108.5 3.5 499 2 A11107 intermalin E limpo
620 108.5 3.5 514 2 H70699 probable ppp prote
621 108.5 3.5 548 1 I37577 islet cell antigen
622 108.5 3.5 662 2 A45155 mucin FIM-C.1 - Af
623 108.5 3.5 698 2 I39713 celB protein - Agr
624 108.5 3.5 710 1 Q0BE22 membrane antigen 9
625 108.5 3.5 740 2 B84741 hypothetrical prote
626 108.5 3.5 756 2 G86308 Similar to disease
627 108.5 3.5 764 2 A35956 thyrotropin recept
628 108.5 3.5 783 1 A38637 Ras interactor RIN
629 108.5 3.5 825 1 A40026 neurotrophin-3 rec
630 108.5 3.5 855 2 C82983 hypothetrical prote
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632 108.5 3.5 1125 2 B41206 microtubule-associ
633 108.5 3.5 1176 2 T49482 hypothetrical prote
634 108.5 3.5 1184 2 G01763 atrophin-1 - huma
635 108.5 3.5 1344 1 A35175 mucin 1 precursor,
636 108.5 3.5 1357 2 T29265 hypothetrical prote
637 108.5 3.5 1487 2 T02850 hypothetrical prote
638 108.5 3.5 3707 2 S18252 heparan sulfate pr
639 108 3.4 348 2 JQ0431 hypothetrical 35.5K
640 108 3.4 409 2 AG0752 flagellar hook-len
641 108 3.4 511 1 VGBE1K glycoprotein C - h
642 108 3.4 542 2 I39540 chitinase (EC 3.2.
643 108 3.4 544 2 T17547 proline-rich prote
644 108 3.4 550 2 T36746 probable serine/th
645 108 3.4 638 1 XXAV dihydrolipoamide S
646 108 3.4 741 2 T05250 probable disease r
647 108 3.4 862 2 S43922 versican - pig-tai
648 108 3.4 996 2 J80237 apolipoprotein E r
649 108 3.4 1017 2 T31354 probable potassium
650 108 3.4 1217 2 T51140 disease resistance
651 108 3.4 1217 2 T51141 disease resistance
652 108 3.4 2783 1 A41948 alpha-fetoprotein
653 108 3.4 3511 2 A59295 unconventional myo
654 108 3.4 4613 2 T17409 polyketide synthas
655 108 3.4 7576 2 T17428 FX506 polyketide s
656 107.5 3.4 363 2 H87702 hypothetrical prote
657 107.5 3.4 369 2 S20500 hydroxyproline-ric
658 107.5 3.4 414 2 C96770 hypothetrical prote
659 107.5 3.4 427 2 S74211 PAS-6/7 protein pr
660 107.5 3.4 536 2 H71563 hypothetrical prote
661 107.5 3.4 604 2 S25203 strmr protein - Str
662 107.5 3.4 655 2 G96524 protein TINI5.9 [i
663 107.5 3.4 832 2 A31246 neurogenic protein
664 107.5 3.4 880 2 S00670 neurogenic repetit
665 107.5 3.4 881 2 B98320 cellulose synthase
666 107.5 3.4 1009 2 T45645 receptor kinase-11
667 107.5 3.4 1099 2 A56155 tumor suppressor p
668 107.5 3.4 1206 2 S24407 formin isoform IV
669 107.5 3.4 1324 2 S52863 DNA-binding protei
670 107.5 3.4 1468 2 S11515 formin - mouse
671 107.5 3.4 3534 2 T42567 tegument protein 2
672 107 3.4 176 1 A46606 platelet glycoprot
673 107 3.4 228 2 S53504 extensin-like prot
674 107 3.4 273 2 A28512 fibronectin - chic
675 107 3.4 354 2 A48931 transmembrane glyc
676 107 3.4 358 1 WMBE38 infected cell prot
677 107 3.4 416 1 SKXLAG dermal gland prote
678 107 3.4 447 2 A39321 mucin - rat (fragm
679 107 3.4 452 2 C41602 transcription fact
680 107 3.4 518 2 F75460 hypothetrical prote
681 107 3.4 615 1 KFHU12 coagulation factor
682 107 3.4 650 2 S59630 dysstroglycan alfa
683 107 3.4 840 1 S69204 pheromone response
684 107 3.4 915 2 T12526 hypothetrical prote
685 107 3.4 1063 1 GNWVR4 structural polypro
686 107 3.4 1376 2 G00043 osteonidogen - hum

687	107	3.4	1389	2	I58157	periaxin - rat	760	105	3.3	1133	2	A54164	sterol regulatory
688	107	3.4	2723	2	T03221	probable polyketid	761	105	3.3	1135	2	T30561	Scythe protein - A
689	107	3.4	7463	2	T36248	CDA peptidase synthe	762	105	3.3	1136	2	S57845	protein-tyrosine k
690	106.5	3.4	304	2	A32993	transcription fact	763	105	3.3	1456	2	T01397	LRR gag/pol polypr
691	106.5	3.4	353	2	A41558	N-syndecan - rat (764	105	3.3	1658	2	D75489	hypothetical prote
692	106.5	3.4	505	2	B46629	mucin 6, gastric (765	105	3.3	1844	2	S01956	hypothetical prote
693	106.5	3.4	509	2	D86911	conserved hypoteth	766	105	3.3	2133	2	T30637	hypothetical prote
694	106.5	3.4	509	2	T10013	probable phosphopr	767	105	3.3	2409	1	A60979	variscan precursor
695	106.5	3.4	517	2	AD1570	internalin, probab	768	105	3.3	2769	1	UIBO	thyroglobulin prec
696	106.5	3.4	620	2	S06733	hydroxyproline-ric	769	104.5	3.3	329	2	T17033	leucine rich repea
697	106.5	3.4	827	2	AC2963	celB protein [impo	770	104.5	3.3	407	2	C70816	hypothetical prote
698	106.5	3.4	925	2	H96638	protein tif9.20 [i	771	104.5	3.3	464	2	T35943	probable hydrolyti
699	106.5	3.4	998	2	C75489	conserved hypoteth	772	104.5	3.3	530	2	T32812	hypothetical prote
700	106.5	3.4	1003	2	T13856	ksr protein-fui	773	104.5	3.3	639	2	G02919	transcription fact
701	106.5	3.4	1161	2	S57180	probable membrane	774	104.5	3.3	662	2	T04856	hypothetical prote
702	106.5	3.4	1184	2	S08032	atrophin-1 - human	775	104.5	3.3	700	2	A42395	lutropin receptor
703	106.5	3.4	1305	2	AB0168	probable cell divi	776	104.5	3.3	707	1	A34458	gelatinase B (EC 3
704	106.5	3.4	1442	2	T42607	transcription acti	777	104.5	3.3	707	1	A53796	probable ABC trans
705	106.5	3.4	1892	2	T18314	hypothetical prote	778	104.5	3.3	744	2	T35192	hypothetical prote
706	106.5	3.4	2090	2	S26058	probable transform	779	104.5	3.3	755	2	T20950	LRR receptor 1 pre
707	106.5	3.4	2453	2	S60254	nuclear receptor c	780	104.5	3.3	909	1	QRXLH1	kinesin-related pr
708	106	3.4	135	2	T43996	AtAGP4 - Arabidops	781	104.5	3.3	960	1	S28262	delta-crystallin/E
709	106	3.4	167	2	A33532	mucin SMUC-40 - hu	782	104.5	3.3	1117	2	JC4934	hypothetical prote
710	106	3.4	216	2	I51920	chitinase (EC 3.2.	783	104.5	3.3	1194	2	E96624	nephlin - human
711	106	3.4	287	2	S65765	mucin - rhesus mac	784	104.5	3.3	1241	2	T37190	hypothetical prote
712	106	3.4	405	2	S78691	flagellar hook-len	785	104.5	3.3	1505	2	JC4851	hypoxia-inducible
713	106	3.4	431	2	S47538	acrosin (EC 3.4.21	786	104.5	3.3	1851	2	T19964	hypothetical prote
714	106	3.4	435	2	D41602	transcription fact	787	104.5	3.3	1898	2	S46216	leukocyte antigen-
715	106	3.4	443	2	B39794	transcription fact	788	104.5	3.3	2117	2	T36180	CDA peptidase synthe
716	106	3.4	449	2	A24993	cellulase (EC 3.2.	789	104	3.3	232	2	A60095	larval glue protei
717	106	3.4	567	2	A45977	Rab geranylgeranyl	790	104	3.3	306	2	I49139	lymphotoxin-beta -
718	106	3.4	666	2	B70803	hypothetical prote	791	104	3.3	318	2	B64900	hypothetical prote
719	106	3.4	701	2	D48613	gag polyprotein -	792	104	3.3	326	2	A46676	CD68 homolog macro
720	106	3.4	818	2	T01105	disease resistance	793	104	3.3	332	2	S43988	protein phosphatas
721	106	3.4	822	2	T51049	related to nucleol	794	104	3.3	360	2	S68209	sds22 protein homo
722	106	3.4	850	2	S56015	gastric mucin MUC5	795	104	3.3	365	2	A39481	serum response fac
723	106	3.4	901	2	A49227	sialidase - Actino	796	104	3.3	426	2	D88103	protein W10G11.6 l
724	106	3.4	914	2	T17233	hypothetical prote	797	104	3.3	440	2	I49681	glycerolaldehyde-3-p
725	106	3.4	1064	2	A40136	fibropellin Ia - s	798	104	3.3	470	2	S36536	myosin-binding pro
726	106	3.4	1603	2	A48613	gag/pol polyprotei	799	104	3.3	537	2	A46611	chitinase (EC 3.2.
727	106	3.4	1958	2	D40505	hypothetical prote	800	104	3.3	538	2	S65764	chitinase (EC 3.2.
728	106	3.4	2554	1	TVPF7L	kinase-related pro	801	104	3.3	593	2	S49525	glycoprotein G - s
729	106	3.4	3338	2	T42761	Basoon protein -	802	104	3.3	712	1	I46031	gelatinase B (EC 3
730	105.5	3.4	395	2	T01392	leucine-rich repea	803	104	3.3	895	2	S20582	dystrophin-associa
731	105.5	3.4	486	2	A41537	DNA-binding protei	804	104	3.3	927	2	T24031	hypothetical prote
732	105.5	3.4	510	2	A42750	insulinoma-associa	805	104	3.3	1045	2	T16275	hypothetical prote
733	105.5	3.4	668	2	T05257	probable disease r	806	104	3.3	1547	2	T28657	blackjack protein,
734	105.5	3.4	688	2	T04568	protein kinase hom	807	104	3.3	1575	2	S68448	synaptotagmin, 170K
735	105.5	3.4	695	2	S62400	amphiphysin (clone	808	104	3.3	1711	2	T31337	1,4-beta-glucanase
736	105.5	3.4	772	2	T13078	KIAA0992 protein -	809	104	3.3	1744	2	A54970	tensin, cardiac mu
737	105.5	3.4	780	2	A48143	HF-1 regulatory el	810	104	3.3	3507	2	T34513	hypothetical prote
738	105.5	3.4	952	2	S32954	hypothetical prote	811	103.5	3.3	206	1	NBHUIB	platelet glycoprot
739	105.5	3.4	1132	2	A35098	MHC class III hist	812	103.5	3.3	264	2	PQ0478	pistil extensin-li
740	105.5	3.4	1172	2	T00065	hypothetical prote	813	103.5	3.3	281	2	D70845	hypothetical prote
741	105.5	3.4	1621	2	T15264	hypothetical prote	814	103.5	3.3	393	2	PQ0479	pistil extensin-li
742	105.5	3.4	1712	2	A38261	masking protein pr	815	103.5	3.3	411	1	I55604	platelet glycoprot
743	105.5	3.4	1839	1	RRWPEM	genome polyprotein	816	103.5	3.3	419	2	T49252	hypothetical prote
744	105.5	3.4	2477	2	S14428	fibronectin precu	817	103.5	3.3	444	1	A39794	transcription fact
745	105.5	3.4	3033	1	JQ1303	genome polyprotein	818	103.5	3.3	489	2	F75591	P49 secreted prote
746	105	3.3	349	2	T05857	hypothetical prote	819	103.5	3.3	625	2	A26456	nicotinic acetylch
747	105	3.3	422	2	I37891	interleukin-11 rec	820	103.5	3.3	654	2	T33044	hypothetical prote
748	105	3.3	454	2	E75291	probable cell wall	821	103.5	3.3	889	2	F96637	hypothetical prote
749	105	3.3	460	2	T33110	hypothetical prote	822	103.5	3.3	898	2	T20123	hypothetical prote
750	105	3.3	486	1	A57601	transcription fact	823	103.5	3.3	968	2	T00353	hypothetical prote
751	105	3.3	511	1	VGBEF4	glycoprotein C - h	824	103.5	3.3	975	2	I48974	receptor-protein t
752	105	3.3	566	2	T34842	probable transferra	825	103.5	3.3	980	2	S54986	regulatory protein
753	105	3.3	620	2	A70525	hypothetical prote	826	103.5	3.3	1020	2	A29355	fibronectin - chic
754	105	3.3	658	2	T08153	cysteine proteinas	827	103.5	3.3	1144	2	A54810	TMV resistance pro
755	105	3.3	730	2	JC1456	gelatinase B (EC 3	828	103.5	3.3	1171	2	T35548	hypothetical prote
756	105	3.3	764	2	JCS5643	thyroid stimulat	829	103.5	3.3	1268	2	T31420	C-terminal domain
757	105	3.3	847	1	A53800	mixed-lineage prot	830	103.5	3.3	1590	2	B86398	protein T7N9.24 [i
758	105	3.3	895	2	I54343	diastroglycan - hum	831	103.5	3.3	1603	2	S23810	collagen alpha 1(X
759	105	3.3	976	2	A36355	protein-tyrosine k	832	103.5	3.3	1638	2	A42091	transcription acti

979	101	3.2	1367	2	T33819	hypothetical prote	1052	99.5	3.2	352	2	S05500	Ig alpha-1 chain C
980	101	3.2	1513	2	A54895	mucin 2, intestina	1053	99.5	3.2	353	1	AlHU	Ig alpha-1 chain C
981	101	3.2	1792	2	A57075	censin - chicken (1054	99.5	3.2	353	2	S36438	EPF1 protein - hyd
982	101	3.2	2946	2	T15840	hypothetical prote	1055	99.5	3.2	375	1	TDH0M4	monocyte surface g
983	101	3.2	3176	2	C6673A	collagen alpha 3(V	1056	99.5	3.2	383	1	VBEBKG	glycoprotein precu
984	100.5	3.2	138	2	D36715	protein F4N2.10 [i	1057	99.5	3.2	387	2	B49175	Motch A protein -
985	100.5	3.2	262	2	T33408	hypothetical prote	1058	99.5	3.2	392	2	B48423	homeotic protein e
986	100.5	3.2	262	2	E88400	hypothetical prote	1059	99.5	3.2	393	1	VBED2	glycoprotein D - h
987	100.5	3.2	269	2	T26957	hypothetical prote	1060	99.5	3.2	420	2	T46910	hypothetical prote
988	100.5	3.2	274	2	T46041	hypothetical prote	1061	99.5	3.2	451	2	JC4199	heat-shock protein
989	100.5	3.2	283	2	E88597	protein Y47D3B.6 [1062	99.5	3.2	476	1	C70986	probable serine/th
990	100.5	3.2	314	2	T48514	hypothetical prote	1063	99.5	3.2	491	2	F70699	probable pbpA prot
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat	1064	99.5	3.2	530	2	S52215	hypothetical prote
992	100.5	3.2	401	2	S65138	glycoprotein antiq	1065	99.5	3.2	539	2	T28770	hypothetical prote
993	100.5	3.2	440	2	JC7807	Wiskott-Aldrich sy	1066	99.5	3.2	647	2	T43952	hypothetical prote
994	100.5	3.2	504	2	AG2373	hypothetical prote	1067	99.5	3.2	665	2	S62328	kinesin-like DNA b
995	100.5	3.2	512	2	S56745	mucin (clone pGM31	1068	99.5	3.2	702	2	A86383	76.4K protein kina
996	100.5	3.2	504	2	E59437	F02569.2 protein [1069	99.5	3.2	802	2	T24293	hypothetical prote
997	100.5	3.2	597	2	J00107	hypothetical 66K p	1070	99.5	3.2	851	2	AD1427	internalin, probab
998	100.5	3.2	677	2	T39713	zinc finger protei	1071	99.5	3.2	853	1	IJBONC	neural cell adhesi
999	100.5	3.2	798	2	T34248	hypothetical prote	1072	99.5	3.2	886	2	T35469	probable ATP /GTP-
1000	100.5	3.2	906	2	A43817	transforming prote	1073	99.5	3.2	903	2	T19209	probable protein k
1001	100.5	3.2	975	2	S33121	homeotic protein C	1074	99.5	3.2	949	2	T24294	hypothetical prote
1002	100.5	3.2	1024	2	T27631	homeotic protein k	1075	99.5	3.2	958	2	E82994	glycine cleavage s
1003	100.5	3.2	1030	2	H88859	hypothetical prote	1076	99.5	3.2	961	1	TSHUP4	thrombospondin 4 p
1004	100.5	3.2	1106	1	TVHUGL	transforming prote	1077	99.5	3.2	1013	2	T33470	hypothetical prote
1005	100.5	3.2	1131	2	F96662	hypothetical prote	1078	99.5	3.2	1016	2	T41720	hypothetical prote
1006	100.5	3.2	1138	1	S24066	protein-tyrosine k	1079	99.5	3.2	1056	2	A53767	mucin MUC5B, trach
1007	100.5	3.2	1220	2	T48928	disease resistance	1080	99.5	3.2	1122	2	T47424	hypothetical prote
1008	100.5	3.2	1273	2	S58782	SEC31 protein - Ye	1081	99.5	3.2	1220	2	T06403	resistance complex
1009	100.5	3.2	1323	2	T30253	spalt protein - mo	1082	99.5	3.2	1390	2	T31353	polyprotein - Arab
1010	100.5	3.2	2327	2	T42630	aggreca - bovine	1083	99.5	3.2	1473	2	T31422	C-terminal domain-
1011	100.5	3.2	2562	2	T42666	xin protein - chic	1084	99.5	3.2	1742	2	T17120	cellulase (EC 3.2.
1012	100.5	3.2	3562	2	A47171	chondroitin sulfat	1085	99.5	3.2	3869	2	A48205	All-1 protein +GTE
1013	100.5	3.2	4548	1	S00657	apoptein(a) (EC	1086	99	3.2	154	2	PQ0476	pistil extensin-li
1014	100	3.2	230	2	A56210	neu differentiatio	1087	99	3.2	214	2	T09854	proline-rich cell
1015	100	3.2	311	2	B86211	hypothetical prote	1088	99	3.2	307	1	GSFF3	salivary glue prot
1016	100	3.2	334	2	G02409	protein kinase C-b	1089	99	3.2	329	2	B41344	lutropin-choriogon
1017	100	3.2	366	2	S61796	T-cell-specific tr	1090	99	3.2	329	2	D41344	lutropin-choriogon
1018	100	3.2	367	2	A33950	yopM protein - Yer	1091	99	3.2	331	2	C41344	lutropin-choriogon
1019	100	3.2	474	2	S15921	protein TPX-VT3 -	1092	99	3.2	358	2	T01296	leucine-rich repea
1020	100	3.2	476	2	C39481	serum response fac	1093	99	3.2	415	1	A34170	acrosin (EC 3.4.21
1021	100	3.2	510	2	H84824	En/Spm-like transp	1094	99	3.2	428	2	S45361	LRR47 protein - fr
1022	100	3.2	535	2	T17212	hypothetical prote	1095	99	3.2	447	2	T34992	probable lipoprote
1023	100	3.2	549	2	C87719	protein R119.6 [im	1096	99	3.2	466	2	T06416	cysteine proteinas
1024	100	3.2	556	2	T07040	probable PPE prote	1097	99	3.2	511	2	AC0941	probable ABC trans
1025	100	3.2	562	2	S75308	DNA ligase (BC 6.5	1098	99	3.2	543	2	S25128	61K protein - Auto
1026	100	3.2	596	2	G75457	tetratricopeptide	1099	99	3.2	564	2	I53106	gene gli protein -
1027	100	3.2	628	2	S44138	polyadenylate-bind	1100	99	3.2	569	2	F75381	probable two-compo
1028	100	3.2	673	2	AF1143	internalin protein	1101	99	3.2	616	2	C75588	conserved hypothet
1029	100	3.2	698	2	T51915	hypothetical prote	1102	99	3.2	638	2	T51383	receptor protein k
1030	100	3.2	698	2	T17261	hypothetical prote	1103	99	3.2	641	2	C84726	probable receptor-
1031	100	3.2	699	2	T09069	probable cAMP-resp	1104	99	3.2	686	2	F96542	probable protein k
1032	100	3.2	713	2	T44447	neuregulin-3 [impo	1105	99	3.2	696	2	A41344	lutropin-choriogon
1033	100	3.2	725	2	T01268	leucine-rich repea	1106	99	3.2	701	2	S61239	hypothetical prote
1034	100	3.2	756	2	C87432	hypothetical prote	1107	99	3.2	770	1	S30233	transcription fact
1035	100	3.2	776	2	A46583	neuroendocrine-Spe	1108	99	3.2	814	2	JC7389	thyroid scintulatin
1036	100	3.2	881	2	T01269	serine/threonine-s	1109	99	3.2	860	2	C86203	hypothetical prote
1037	100	3.2	1109	2	C84545	probable disease r	1110	99	3.2	940	2	H86420	probable receptor-
1038	100	3.2	1161	2	T45294	hypothetical prote	1111	99	3.2	963	2	T19140	hypothetical prote
1039	100	3.2	1182	2	T48378	hairless protein -	1112	99	3.2	1000	2	C82630	serine proteinase
1040	100	3.2	1240	2	T06404	resistance complex	1113	99	3.2	1097	2	T49187	hypothetical prote
1041	100	3.2	1420	2	T37781	probable cytoskele	1114	99	3.2	1147	2	T42627	ADP-ribosylation f
1042	100	3.2	1687	2	T30176	EGF repeat transme	1115	99	3.2	1217	2	T52348	disease resistance
1043	100	3.2	1791	2	T02345	hypothetical prote	1116	99	3.2	1317	2	T03748	apoptosis associat
1044	100	3.2	1802	2	T00020	bacterial blight-r	1117	99	3.2	1405	2	T04426	hypothetical prote
1045	100	3.2	1897	1	TDHULK	leukocyte antigen-	1118	99	3.2	1532	2	A61262	collagen alpha 1(X
1046	100	3.2	2459	2	AF2136	peptide synthetase	1119	99	3.2	1538	2	E70874	probable pbpB prot
1047	99.5	3.2	108	2	S08315	cell wall protein	1120	99	3.2	1694	2	S50065	sialoadhesin - mou
1048	99.5	3.2	177	2	T07642	PEARL1 protein h	1121	99	3.2	1799	1	S44920	Zk688.5 protein -
1049	99.5	3.2	230	2	A44074	probable EGF-like	1122	99	3.2	2029	1	TDFFLK	protein-tyrosine-p
1050	99.5	3.2	280	2	I48713	Phox2 homeodomain	1123	99	3.2	2088	2	E71436	hypothetical prote
1051	99.5	3.2	293	2	C75421	hypothetical prote	1124	99	3.2	6420	2	T30283	polyketide synthas

1125	98.5	3.1	230	2	T22763	hypotheical prote	1198	97.5	3.1	362	2	S22395	fetuin precursor -
1126	98.5	3.1	254	2	D88560	protein F58A4.1 [i	1199	97.5	3.1	429	2	JC4965	elk1 protein - mou
1127	98.5	3.1	342	2	T77461	luteinizing hormon	1200	97.5	3.1	460	2	T23087	hypotheical prote
1128	98.5	3.1	349	2	T15432	hypotheical prote	1201	97.5	3.1	464	2	S22697	extensin - Volvox
1129	98.5	3.1	379	2	S50135	larval glue protei	1202	97.5	3.1	497	2	F83634	hypotheical prote
1130	98.5	3.1	385	2	T18180	proline-rich prote	1203	97.5	3.1	511	2	T43282	alp21 protein - fi
1131	98.5	3.1	393	2	S62335	171-7 protein - fr	1204	97.5	3.1	521	2	S54266	tyrosine decarboxy
1132	98.5	3.1	434	1	A35005	u-plasminogen acti	1205	97.5	3.1	531	2	B55066	glycoprotein gc -
1133	98.5	3.1	464	2	D72653	hypotheical prote	1206	97.5	3.1	563	2	A75594	ferredoxin-nitrite
1134	98.5	3.1	486	2	B39481	serum response fac	1207	97.5	3.1	574	1	A48501	probable protein-1
1135	98.5	3.1	514	2	A44100	cell adhesion mole	1208	97.5	3.1	587	2	T41653	probable transcrip
1136	98.5	3.1	633	2	T47346	receptor protein k	1209	97.5	3.1	614	2	T33149	hypotheical prote
1137	98.5	3.1	700	2	T77463	luteinizing hormon	1210	97.5	3.1	636	2	B70754	probable serine/th
1138	98.5	3.1	700	2	A49744	lutropin-choriogon	1211	97.5	3.1	627	1	JC6534	protein kinase 1 (
1139	98.5	3.1	707	2	A46302	PRB-associated spl	1212	97.5	3.1	627	2	AB0535	hypotheical prote
1140	98.5	3.1	770	2	T22808	hypotheical prote	1213	97.5	3.1	631	1	A36749	transcription fact
1141	98.5	3.1	803	2	F59433	RhOGAP protein lim	1214	97.5	3.1	662	2	D40228	neuraxin II-beta p
1142	98.5	3.1	837	2	A42112	mucin-like peptide	1215	97.5	3.1	676	1	EDB823	immediate-early pr
1143	98.5	3.1	862	2	B88594	protein Y48A6B.11	1216	97.5	3.1	710	2	D96728	hypotheical prote
1144	98.5	3.1	885	2	B86257	NBS/LRR disease re	1217	97.5	3.1	754	2	AC2807	OmpA family protei
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -	1218	97.5	3.1	754	2	B97586	hypotheical prote
1146	98.5	3.1	947	2	T26314	hypotheical prote	1219	97.5	3.1	814	2	G02390	disintegrin-like m
1147	98.5	3.1	1087	2	T31100	probable potassium	1220	97.5	3.1	817	2	S51342	verprolin - yeast
1148	98.5	3.1	1272	2	T30248	fragile X mental r	1221	97.5	3.1	830	2	T17672	chitinase-like pro
1149	98.5	3.1	1281	2	T00346	hypotheical prote	1222	97.5	3.1	893	2	H96651	protein T3P18.19 [
1150	98.5	3.1	1309	2	T00078	probable RNA-direc	1223	97.5	3.1	909	1	A54809	disease resistance
1151	98.5	3.1	1396	2	A44453	translation initia	1224	97.5	3.1	921	2	AE0332	conserved hypothe
1152	98.5	3.1	1774	2	B56101	collagen alpha 1(X	1225	97.5	3.1	929	2	T52517	hypotheical prote
1153	98.5	3.1	2180	2	T29764	hypotheical prote	1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1154	98.5	3.1	2339	2	A42566	omega-conotoxin-se	1227	97.5	3.1	1006	2	G86292	hypotheical prote
1155	98	3.1	182	2	T07641	PEARL1 i protein h	1228	97.5	3.1	1258	2	JC5765	inositol polyphosp
1156	98	3.1	291	2	AF0123	probable antigenic	1229	97.5	3.1	1392	2	T51947	probable transcrip
1157	98	3.1	296	2	A56943	sensory/motor neur	1230	97.5	3.1	1715	2	C40228	neuraxin II-alpha
1158	98	3.1	303	2	S40973	hypotheical prote	1231	97.5	3.1	1748	1	JQ1555	genome polyprotein
1159	98	3.1	352	2	S09266	Ig alpha chain C r	1232	97	3.1	191	2	F84522	probable proline-r
1160	98	3.1	416	1	A42879	advanced glycosyla	1233	97	3.1	238	2	T23867	hypotheical prote
1161	98	3.1	442	2	S50062	cell wall glycopro	1234	97	3.1	238	2	T26419	hypotheical prote
1162	98	3.1	499	2	A12449	hypotheical prote	1235	97	3.1	330	2	T05717	probable extensin
1163	98	3.1	514	2	A56201	transcription fact	1236	97	3.1	355	2	B26883	neural cell adhesi
1164	98	3.1	534	2	S21961	proline-rich prote	1237	97	3.1	357	2	A93364	GDF-1 embryonic gr
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.	1238	97	3.1	379	2	AE3003	conserved hypothe
1166	98	3.1	538	2	T68093	PRR2 delta - human	1239	97	3.1	395	2	A86166	protein F21B7.6 [i
1167	98	3.1	553	1	A70836	hypotheical prote	1240	97	3.1	397	2	T00914	leucine-rich repea
1168	98	3.1	553	1	A42499	mullerian inhibiti	1241	97	3.1	400	1	A28172	spasmolysin precu
1169	98	3.1	560	1	WFHUM	mullerian inhibiti	1242	97	3.1	421	1	S11674	acrosin (EC 3.4.21
1170	98	3.1	605	2	S48940	hypotheical prote	1243	97	3.1	428	1	TVHUEK	transforming prote
1171	98	3.1	614	2	S27962	modulator recognit	1244	97	3.1	452	2	D98280	hypotheical 28.0K
1172	98	3.1	631	2	C89243	protein F28C1.3 [i	1245	97	3.1	459	2	T35317	probable serine/th
1173	98	3.1	631	2	T21471	hypotheical prote	1246	97	3.1	483	2	T02226	NBS-LRR type resis
1174	98	3.1	715	2	S76492	lipoprotein nlpo -	1247	97	3.1	500	2	D97302	hypotheical prote
1175	98	3.1	728	2	H59435	phosphoinositide-3	1248	97	3.1	530	2	G70904	hypotheical prote
1176	98	3.1	750	2	T42614	probable envelope	1249	97	3.1	601	2	D89711	protein P40E10.4 [
1177	98	3.1	788	1	Q0B8E3	HRH1 protein - hu	1250	97	3.1	601	2	T22025	hypotheical prote
1178	98	3.1	856	2	T43631	serine/threonine k	1251	97	3.1	632	2	T02627	hypotheical prote
1179	98	3.1	889	2	C86257	resistance to Pseu	1252	97	3.1	701	1	FOFV1R	gag polyprotein -
1180	98	3.1	896	2	S36326	clathrin assembly	1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1181	98	3.1	1006	2	JC5526	kinase-defective E	1254	97	3.1	966	2	D96662	hypotheical prote
1182	98	3.1	1216	2	T34101	hypotheical prote	1255	97	3.1	967	2	G96637	hypotheical prote
1183	98	3.1	1372	2	T25933	hypotheical prote	1256	97	3.1	1123	2	A39962	kinase-related tra
1184	98	3.1	1522	2	H88380	protein T22P7.3 [i	1257	97	3.1	1214	2	T47438	disease resistance
1185	98	3.1	1873	2	A55645	calcium channel, v	1258	97	3.1	1265	1	A37967	neural cell adhesi
1186	98	3.1	2115	2	S38480	nonstructural prot	1259	97	3.1	1690	2	T35694	ATP dependent DNA
1187	98	3.1	3190	2	T13828	CRPB-binding prote	1260	97	3.1	1734	2	A54602	microtubule-associ
1188	98	3.1	3623	2	T08618	intrinsic factor-B	1261	97	3.1	2055	2	T00093	hypotheical prote
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch	1262	97	3.1	2205	1	GNNY2W	genome polyprotein
1190	98	3.1	3871	2	T22812	hypotheical prote	1263	97	3.1	3034	2	T14119	seven-pass transme
1191	98	3.1	5069	2	T17464	rifamycin polyketi	1264	96.5	3.1	346	2	S19129	proline-rich prote
1192	97.5	3.1	215	2	S55925	probable arabinoga	1265	96.5	3.1	350	2	E75341	peptidyl-prolyl ci
1193	97.5	3.1	266	1	A35037	insulin-like growt	1266	96.5	3.1	419	2	G70602	hypotheical prote
1194	97.5	3.1	268	2	S71830	transcription coac	1267	96.5	3.1	430	2	I48755	msAP1a - mouse
1195	97.5	3.1	277	2	A46241	interferon respons	1268	96.5	3.1	444	2	B63389	transcription fact
1196	97.5	3.1	306	2	T09067	extensin-like prot	1269	96.5	3.1	485	1	S22543	transcription fact
1197	97.5	3.1	338	1	TVMSGFB	transforming prote	1270	96.5	3.1	487	2	F70765	hypotheical prote

1271	96.5	3.1	514	2	A31643	cell adhesion 80K	1344	95.5	3.0	1159	2	I38465	probable potassium
1272	96.5	3.1	528	2	B75310	conserved hypothet	1345	95.5	3.0	1255	2	T031065	diaphanous protein
1273	96.5	3.1	574	2	B35149	ipaH protein - Shi	1346	95.5	3.0	1256	2	T03096	CDO protein - rat
1274	96.5	3.1	598	2	T42070	protein serine/thr	1347	95.5	3.0	1331	2	T49813	related to gastric
1275	96.5	3.1	635	2	T70874	probable membrane	1348	95.5	3.0	1630	2	T00390	KIAA0614 protein -
1276	96.5	3.1	637	2	A75342	hypothetical prote	1349	95.5	3.0	2761	2	T21064	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote	1350	95	3.0	175	2	I38408	neu differentiation
1278	96.5	3.1	654	2	T45017	chemotaxis histidi	1351	95	3.0	227	2	C29149	proline-rich prote
1279	96.5	3.1	669	2	T08827	hypothetical prote	1352	95	3.0	227	2	G70555	hypothetical prote
1280	96.5	3.1	796	2	E86654	hypothetical prote	1353	95	3.0	239	2	S25618	hypothetical prote
1281	96.5	3.1	825	1	EDBEXD	immediate-early pr	1354	95	3.0	241	2	D43273	herregulin precurs
1282	96.5	3.1	1021	2	A86421	Receptor-like seri	1355	95	3.0	273	2	C70551	hypothetical prote
1283	96.5	3.1	1209	2	T00373	hypothetical prote	1356	95	3.0	326	2	A59232	ABA-responsive pro
1284	96.5	3.1	1241	2	T18311	hypothetical prote	1357	95	3.0	338	2	T06336	proline-rich prote
1285	96.5	3.1	1557	2	T02859	probable serine/th	1358	95	3.0	385	1	I39498	GTP cyclohydrolase
1286	96.5	3.1	2282	2	T42717	DNA-binding protei	1359	95	3.0	413	2	T52617	hypothetical prote
1287	96.5	3.1	2352	2	T30201	Notch homolog prot	1360	95	3.0	477	2	S53362	mucin 5AC (clone J
1288	96.5	3.1	25926	1	I38344	titin, cardiac mus	1361	95	3.0	494	1	A29079	lymphocyte surface
1289	96	3.1	214	2	T10737	extensin-like cell	1362	95	3.0	502	2	A55197	Wiskott-Aldrich sy
1290	96	3.1	240	2	A24264	proline-rich prote	1363	95	3.0	636	2	I61718	neu differentiation
1291	96	3.1	287	2	C75494	cell division prot	1364	95	3.0	653	2	E84682	hypothetical prote
1292	96	3.1	346	2	JA0159	cysteine proteinas	1365	95	3.0	662	2	I61722	neu differentiation
1293	96	3.1	445	2	T05887	hypothetical prote	1366	95	3.0	667	2	T17221	hypothetical prote
1294	96	3.1	451	2	D88395	protein F53A3.6 [i	1367	95	3.0	673	2	T48012	hypothetical prote
1295	96	3.1	483	2	S12741	transcription fact	1368	95	3.0	705	2	A35621	spore germination
1296	96	3.1	537	1	F0MVGV	gag polyprotein -	1369	95	3.0	712	2	G02512	interleukin-1 rece
1297	96	3.1	580	2	T43481	probable mucin DKF	1370	95	3.0	760	2	T16726	hypothetical prote
1298	96	3.1	594	2	S33561	ref(2)P protein -	1371	95	3.0	776	2	C96554	unknown protein li
1299	96	3.1	598	2	T48822	hypothetical prote	1372	95	3.0	799	2	T48889	serine/threonine p
1300	96	3.1	635	1	WMBEW6	capsid protein - h	1373	95	3.0	846	2	S52418	GTP-binding regula
1301	96	3.1	858	1	IURTNC	neural cell adhesi	1374	95	3.0	891	2	G84693	probable proline-r
1302	96	3.1	883	2	A96662	hypothetical prote	1375	95	3.0	901	2	A44825	phosphoprotein, sy
1303	96	3.1	907	2	A29951	cell division prot	1376	95	3.0	903	2	S60257	meltin alpha - mo
1304	96	3.1	910	2	H98331	cell division prot	1377	95	3.0	943	2	T34847	probable transcrip
1305	96	3.1	969	2	A75634	MxR-related prote	1378	95	3.0	1024	2	S18251	collagen alpha 1(X
1306	96	3.1	1216	2	T26104	hypothetical prote	1379	95	3.0	1209	2	T13153	brahma associated
1307	96	3.1	1231	2	S30185	insulin receptor s	1380	95	3.0	1324	2	T14070	peptide synthetase
1308	96	3.1	1544	2	E59431	phosphoinositide-b	1381	95	3.0	1474	2	B85188	retrotransposon li
1309	96	3.1	1615	2	B49502	protein-tyrosine-p	1382	95	3.0	1616	2	G70668	polyketide synthas
1310	96	3.1	1737	2	T00209	MEGF8 protein - hu	1383	95	3.0	1731	2	AB3045	ice nucleation pro
1311	96	3.1	1767	2	A49502	protein-tyrosine-p	1384	95	3.0	1731	2	B98241	hypothetical prote
1312	96	3.1	1844	1	IRWPTM	genome polyprotein	1385	95	3.0	1770	2	T18551	safranycin Mxi syn
1313	96	3.1	2529	2	A56923	transcription fact	1386	95	3.0	1806	1	CGHUIE	collagen alpha 1(X
1314	96	3.1	5376	2	T42215	zonadhesin - mouse	1387	95	3.0	2090	2	T30075	hypothetical prote
1315	95.5	3.0	188	2	D29149	proline-rich prote	1388	95	3.0	2148	2	A56011	transcription fact
1316	95.5	3.0	284	2	F95320	conserved hypothet	1389	95	3.0	2274	2	T30258	adenomatous polypo
1317	95.5	3.0	366	1	TDMSM4	monocyte surface g	1390	95	3.0	3084	1	MMMSA	laminin alpha-1 ch
1318	95.5	3.0	382	2	S75823	threonine synthase	1391	94.5	3.0	211	2	T03381	high sulfur zein p
1319	95.5	3.0	384	2	S51796	vasodilator-stimul	1392	94.5	3.0	255	2	B75309	hypothetical prote
1320	95.5	3.0	435	2	T46443	hypothetical prote	1393	94.5	3.0	255	2	S31096	proline-rich prote
1321	95.5	3.0	451	2	S71754	cellular hepatitis	1394	94.5	3.0	270	2	B87649	hypothetical prote
1322	95.5	3.0	479	2	D70676	probable PE protei	1395	94.5	3.0	277	2	I38857	microtubule-associ
1323	95.5	3.0	486	2	AB2975	succinate semialde	1396	94.5	3.0	298	2	H87533	peptidase, M23/M37
1324	95.5	3.0	486	2	A93808	atfK protein (U594	1397	94.5	3.0	301	2	D87684	transcription regu
1325	95.5	3.0	501	2	S76563	hypothetical prote	1398	94.5	3.0	358	2	A61188	probable transcrip
1326	95.5	3.0	507	1	A46713	erythropoietin rec	1399	94.5	3.0	375	2	B82988	hypothetical prote
1327	95.5	3.0	553	2	C75318	hypothetical prote	1400	94.5	3.0	393	2	B82283	conserved hypothet
1328	95.5	3.0	570	2	A48836	fibropellin C prec	1401	94.5	3.0	464	2	A83557	probable amidase P
1329	95.5	3.0	571	2	T43456	hypothetical prote	1402	94.5	3.0	569	2	T19128	hypothetical prote
1330	95.5	3.0	573	2	B70726	probable secD - My	1403	94.5	3.0	630	2	A39344	tumor-associated m
1331	95.5	3.0	624	2	T49366	myocyte-specific e	1404	94.5	3.0	665	2	E75461	probable cell wall
1332	95.5	3.0	630	2	T31798	hypothetical prote	1405	94.5	3.0	708	2	JC4364	gelatinase B (EC 3
1333	95.5	3.0	650	2	S44806	F10S9.6 protein -	1406	94.5	3.0	719	2	T33170	hypothetical prote
1334	95.5	3.0	685	2	C56591	E75 B steroid rece	1407	94.5	3.0	719	2	T33170	tenascin-X - mouse
1335	95.5	3.0	710	1	S70965	serine/threonine-s	1408	94.5	3.0	860	2	I48839	collagen alpha 1(I
1336	95.5	3.0	722	2	T23359	hypothetical prote	1409	94.5	3.0	985	2	T06049	hypothetical prote
1337	95.5	3.0	749	2	B87599	hypothetical prote	1410	94.5	3.0	1006	2	T00050	hypothetical prote
1338	95.5	3.0	790	1	TWHTTT	nerve growth facto	1411	94.5	3.0	1092	2	JN0635	neural cell adhesi
1339	95.5	3.0	880	2	D89756	protein T23E7.2b [1412	94.5	3.0	1191	2	T13850	gene u-shaped prot
1340	95.5	3.0	943	2	E84429	probable receptor-	1413	94.5	3.0	1487	1	EDBEE1	immediate-early pr
1341	95.5	3.0	987	2	A54092	protein-tyrosine k	1414	94.5	3.0	1690	1	CGHUIB	collagen alpha 4(I
1342	95.5	3.0	1027	2	I38759	zinc finger/leucin	1415	94.5	3.0	2062	2	G96602	probable receptor
1343	95.5	3.0	1054	2	A30239	hydroxymethylgluta	1416	94.5	3.0	2302	2	T14328	protein-tyrosine-p

1417 94.5 3.0 2386 1 FNHU fibronectin precu
1418 94.5 3.0 2484 2 T26216 hypothet
1419 94.5 3.0 2607 2 T26215 hypothet
1420 94 3.0 157 2 T02034 early light-induce
1421 94 3.0 263 2 S57346 interleukin 15 rec
1422 94 3.0 277 2 T27564 hypothet
1423 94 3.0 293 2 T22919 hypothet
1424 94 3.0 329 2 T10064 hypothet
1425 94 3.0 338 2 S28004 probable cell surf
1426 94 3.0 346 2 S76923 hypothet
1427 94 3.0 356 2 A96826 T8K14.10 (imported
1428 94 3.0 421 2 T38309 probable cell wall
1429 94 3.0 456 2 A40492 early growth respo
1430 94 3.0 466 2 A36389 transcritpion fact
1431 94 3.0 476 2 B44997 merozoite surface
1432 94 3.0 522 2 S41819 nucleoporin p62 -
1433 94 3.0 559 2 C75286 hypothet
1434 94 3.0 590 2 B36789 hypothet
1435 94 3.0 639 2 I61719 whn protein - rat
1436 94 3.0 648 2 S50856 pectate lyase (EC
1437 94 3.0 677 2 JC7303 serine/threonine-s
1438 94 3.0 693 1 A41090 hypothet
1439 94 3.0 791 2 S67265 hypothet
1440 94 3.0 811 2 T36581 probable transmem
1441 94 3.0 862 2 S51493 major nitrogen reg
1442 94 3.0 865 1 D70986 probable ABC trans
1443 94 3.0 878 1 A40091 interleukin-3 rece
1444 94 3.0 898 2 A40114 fasciclin II precu
1445 94 3.0 918 2 A43361 scavenger receptor
1446 94 3.0 927 2 A48085 transcritpion fact
1447 94 3.0 939 2 C70876 hypothet
1448 94 3.0 979 2 A70848 probable membrane
1449 94 3.0 1007 2 G96606 disease resistance
1450 94 3.0 1137 2 G70868 probable regulator
1451 94 3.0 1236 2 E70977 hypothet
1452 94 3.0 1320 2 J56630 TCO1 protein - mo
1453 94 3.0 1331 2 A48954 mannann endo-1,4-be
1454 94 3.0 1335 2 T18289 rAGAP protein - s
1455 94 3.0 1429 2 T13720 gene expanded prot
1456 94 3.0 1549 2 T11974 glutamate synthase
1457 94 3.0 1560 2 T00080 hypothet
1458 94 3.0 2153 2 T30074 hypothet
1459 93.5 3.0 172 2 D41132 collagen-related p
1460 93.5 3.0 278 2 T27610 hypothet
1461 93.5 3.0 299 2 G70784 probable mmp3 pro
1462 93.5 3.0 305 2 T46721 hypothet
1463 93.5 3.0 352 2 T06482 probable cell wall
1464 93.5 3.0 362 2 S61924 cyst wall protein
1465 93.5 3.0 391 2 I50702 transcritpion fact
1466 93.5 3.0 458 2 B87335 hypothet
1467 93.5 3.0 461 1 A35356 tumor necrosis fac
1468 93.5 3.0 490 2 AG1107 internalin G [impo
1469 93.5 3.0 522 2 T36501 probable serine/th
1470 93.5 3.0 530 2 A53437 poliovirus recepto
1471 93.5 3.0 556 2 T42100 serine/threonine p
1472 93.5 3.0 577 2 T18116 hypothet
1473 93.5 3.0 662 2 T46005 receptor-like prot
1474 93.5 3.0 691 2 B75622 hypothet
1475 93.5 3.0 718 2 T05840 hypothet
1476 93.5 3.0 719 2 F96577 subtilisin-like pr
1477 93.5 3.0 854 2 A96574 hypothet
1478 93.5 3.0 909 1 QRXL22 LDL receptor 2 pre
1479 93.5 3.0 919 2 F83257 hypothet
1480 93.5 3.0 998 2 T35745 probable ATP-bind
1481 93.5 3.0 1121 2 JC7323 WD-repeat protein
1482 93.5 3.0 2109 2 B89066 protein H05009.1 [
1483 93.5 3.0 2150 2 T32497 hypothet
1484 93.5 3.0 2295 2 C88369 protein unc-52 [im
1485 93.5 3.0 3375 2 T19821 hypothet
1486 93 3.0 209 2 T02262 high-methionine d-
1487 93 3.0 221 2 T07079 leucine-rich repea
1488 93 3.0 235 2 FC2022 mucin like protein

1490 93 3.0 328 2 S01359 salivary glue prot
1491 93 3.0 338 2 S38030 suppressor protein
1492 93 3.0 384 2 H70580 hypothet
1493 93 3.0 413 2 AH2743 conserved hypothet
1494 93 3.0 416 2 G57524 hypothet
1495 93 3.0 438 2 G87675 arylesterase-relat
1496 93 3.0 453 2 B42093 serum response fac
1497 93 3.0 465 2 B82515 alpha-L-fucosidase
1498 93 3.0 558 2 T50742 protoporphyrin IX
1499 93 3.0 560 1 JC4795 plasma hyaluronan-
1500 93 3.0 586 2 H86914 conserved hypothet

ALIGNMENTS

RESULT 1

JC5239 insulin-like growth factor acid-labile chain - baboon

C;Species: Papio sp. (baboon)

C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997

C;Accession: JC5239

E;Delhanty, P.; Baxter, R.C.

Biochem. Biophys. Res. Commun. 227, 897-902, 1996

A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like

A;Reference number: JC5239; MUID:97040714; PMID:8886027

A;Contents: liver

A;Accession: JC5239

A;Molecule type: mRNA

A;Residues: 1-605

A;Cross-references: UNIPARC:UPI000000D50E

C;Comment: This factor is structurally related to proinsulin and have insuline-like meta

Query Match 10.3%; Score 322; DB 2; Length 605;

Best Local Similarity 36.2%; Pred. No. 2e-11;

Matches 100; Conservative 39; Mismatches 97; Indels 40; Gaps 11;

Qy 7 LLLPLLLL--LALG-----PGVQC-----CPSCQCQSOPQ-----TVFCTARQGT 45
Db 8 LALALLLSVALGPRSLGAEFGTGAEGPACATCACSYDDEVNELSVFCSSRLNR 67
Qy 46 VPRDVPDTVGLYVFENGITMLDASSFAGLGLQLLDLSONQIASRLPRLLL----- 98
Db 68 LPDGIPOGTQALWLDNNLSSIPPAAPFNLSLAFLNLQGGQLGSLR-PQALLGLENLCH 126
Qy 99 LDLSHNSLLALEPGILDITANVEALRLAGLG---LQDDEGLFSLRLMHLDVDNQLER 155
Db 127 LHLERQRLSLAVGTF--AYTPALALGLGNNRLSLRLEDGLFEGGLNLDNLGWSLAV 184
Qy 156 VP-PVIRGLRLRLAGNTRIAQLRPEDLAGLALQELDVNSLSLQALPGDLSGLFPR 214
Db 185 LPDAAFGLGGLRELVLVAGN-RLAYLPALFSGLAELRELDLSRNAURLAKANVFAQLPR 243
Qy 215 LRLAARPNFNCVPLSWFG-----PWVRESHVTLA 246
Db 244 LQKLYLDRLNLIAAVAFGLKALRWLDLSHRVA 279

RESULT 2

A41915

insulin-like growth factor-binding complex acid-labile chain precursor - human

N;Alternate names: Acid-Labile Subunit (ALS)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A41915

R;Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.

Mol. Endocrinol. 6, 870-876, 1992

A;Title: Structure and functional expression of the acid-labile subunit of the insulin-li

A;Reference number: A41915; MUID:92357025; PMID:1379671

A;Accession: A41915

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-605 <LEO>

A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)
F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>

Query Match 9.6%; Score 302; DB 2; Length 605;
Best Local Similarity 35.5%; Pred. No. 2.9e-10;
Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;

QY 7 LLLPLLLL--LALG-----PGVQG-----CPSGCQSQPQ-----TFCTARQTT 45
DB 8 LALALLLSWALGPRSLLEGADPGTGEAGPACPAACVCSYDDADELSFCSSRLTR 67
QY 46 VPRDVPPTVGVVFNIGITMDASSFAGLPGLQLLDSQNIASLRPLRLLL----- 98
DB 68 LPDGVFGTQALWLDGNNLSVPPAFAQNLSSGLFNLQGGQLGSLP-QALLGLENLCH 126
QY 99 LDLSHNSLALPEGLTDTANVEALRAGLG---LQQLDEGLFSRLNLHLDVSDNLER 155
DB 127 LHLENNQRLSLALGTF--AHTPALASLGUNNRLSRLEDGLFEGLSGLWLDNLGWSLAV 184
QY 156 VP-PIVIRGLGRLTRLAGNTRIAQLRPEDLAGLAAQLDELVDVNSLQALPGDLSGLFPR 214
DB 185 LPDAAFRGLSRLVLVLAGN-RLAYLQPALFSLGLAELRELDLSRNALRAIKANVFVQLPR 243
QY 215 LRLLAARNPNCVCLPSWFG-----PWRESHVTLA 246
DB 244 LQKGLDRNLRTAAVAPGAPGLGKALRWLDLSHRVA 279

RESULT 3
NBHUIA
platelet glycoprotein Ib alpha chain precursor - human
N;Alternate names: membrane glycoprotein Ib alpha chain
N;Contains: glycosialicin
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102
R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987
A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p
A;Reference number: A94174; MUID:87289655; PMID:3303030
A;Accession: A94174
A;Molecule type: mRNA
A;Residues: 1-626 <LOP>
A;Cross-references: UNIPROT:P07359; UNIPARC:UPI000012B962; GB:J02940; NID:g183499; PIDN:
R;Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J.
Thromb. Haemost. 61, 448-453, 1989
A;Title: Isolation and characterization of human blood platelet mRNA and construction of
d cloning of a GPIb coding cDNA insert.
A;Reference number: A60435; MUID:90020160; PMID:2799758
A;Accession: A60435
A;Molecule type: mRNA
A;Residues: 207-467 <WIC>
A;Cross-references: UNIPARC:UPI0000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet mem
A;Reference number: A94173; MUID:87289654; PMID:3497398
A;Accession: A94173
A;Molecule type: protein
A;Residues: 17-315 <WIT>
A;Cross-references: UNIPARC:UPI0000174312
R;Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.
Eur. J. Biochem. 199, 389-393, 1991
A;Title: Identification of the disulphide bonds in human platelet glycosialicin.
A;Reference number: S16945; MUID:91301149; PMID:2070794
A;Accession: S16945
A;Status: preliminary
A;Molecule type: protein
A;Residues: 224-227;262-270;277-282 <HES>
A;Cross-references: UNIPARC:UPI0000174313; UNIPARC:UPI0000174314; UNIPARC:UPI0000174315
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t
ations.
A;Reference number: I55355; MUID:92250564; PMID:1577776
A;Accession: I55355
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 412-427 <RES>
A;Cross-references: UNIPARC:UPI0000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:
A;Note: variant D
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates
C;Comment: Platelet activation apparently involves disruption of the macromolecular comp
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un
C;Comment: Glycosialicin, which is approximately coextensive with the extracellular part c
C;Genetics:
A;Gene: GDB:GP1BA; GPIB
A;Cross-references: GDB:118806; OMIM:231200
A;Map position: 17pter-17p12
C;Complex: heterodimer with platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r
C;Superfamily: platelet glycoprotein Ib alpha chain; glycoprotein; platelet membrane; tandem repe
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repe
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>
F:48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:379-430/Region: proline/threonine-rich 9-residue repeats
F:502-540/Domain: transmembrane #status predicted <TRM>
F:541-626/Domain: intracellular #status predicted <INT>
F:37,175/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:308/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 9.0%; Score 282; DB 1; Length 626;
Best Local Similarity 24.0%; Pred. No. 4.4e-09;
Matches 160; Conservative 72; Mismatches 244; Indels 190; Gaps 26;

QY 9 LPLLLLLALGPGVQCGPCSGCQSQPQOT---VFCTARQGTTPRDPVPPDTVGLYVFEN--- 62
DB 1 MPLLLLLLLLPLPHPHPICEVSKVASHLEVNCCKRNLTALPPDLPKDTTILHSENLLY 60
QY 63 -----GITMLDASSF-----AGLPGLQLLDLSQNIASL-----RLPRLLL 98
DB 61 TFSLATLMPYRLTQLNDRCELTKLQVDGTLFVLGTLDSLHNLQSLPLLGQTLPALTV 120
QY 99 LDLSHNSLALPEGLT-DTANVEALRAGLGQLQQLDEGLFSRLNLHLDVSDNLERVP 157
DB 121 LDVSGNRLTSLPLGALRGGLGELQELYLKGNKLTLPGLLTPTPKLEKLSANNLTLP 180
QY 158 P-VIRGLRGLTRLRAGNTRIAQLRPEDLAGLAAQLDELVDVNSLQALPGDLSG--LPRP 214
DB 181 AGLINGLENLDTLLIQEN-----SLYTIKPGFGSHLLPF 215

Matches 127; Conservative 56; Mismatches 207; Indels 102; Gaps 16;

QY 6 PLLPLLLLLALGPGVQCPCGQCQSQPTVCTARQGTTPRDPVPPDVTGLYFENGIT 65
DB 16 PELWLLWAAAWRLGATACPALCTCT-GTTVDCHGTGLQAIKPIKPRNTERLELNGNIT 74
QY 66 MLDASSFAGLPGQLQLDLSQNOIASLRPLRLLLDLSHNSLLALEPGIL-DTANVEALRL 124
DB 75 RIHKNDFAGLKQLRVLMENQIG-----AVERGAFDDMKELERLRL 116
QY 125 AGLGLQQLDEGLFSRLRLHDLVSDNQLERVP-PVIRGLRGLRLRAGNTRIAQLRPE 183
DB 117 NRNQQLPELLFQNNQALSRLLDSENSLQAVPRKAPRGATDLKNQLQDKN-QISCTIEG 175
QY 184 DIAGLAALQELDVSNLSLQALPGDLSGLFPRRLILAAARNPFCVPLSWFGPWRSHV 243
DB 176 AFRALRGLEVLTLNNNTTTPVSSFNHMPKLRTPRLSHNHLFCDCHLAWLSQWLRO-RP 234
QY 244 TLASPEETRCHPPKPNAGRLLELDYADGCPATTTTATVTPTRPVVREPTALSSSLAPT 303
DB 235 TIGL--FTQCGSPASRLGNVAEVOKSEFSCGQGEAAQVPA-----CTLSSGSCPA 284
QY 304 WLSPTAPATEAPSPSTAPPTVGPVPQPQ-----DCPPSTCLNGGTCHLG----- 348
DB 285 MCSCSNGIVDCRGKGLTAIPANLPETMTETIRLELNGIKSIPP-----GAFSPYR 333
QY 349 -----TRHHLACLCPGFTGLYCESQMGQTRPSPTVTPRPRRSITLGIPEVS--PT 399
DB 334 KLRRIIDLNNQIAETAPDAFOGL-----RSLSVLVYGNKITDPLR 374
QY 400 SLRVGLQRYLQSSVQLASRLTYRNLSPD--KRLVTLRPA-----SLAEVTVTQL 450
DB 375 GVGGLY-----TQQLLLNANKINCIRPDFAQDLQNLSSLYDNKIQSLAKGTFTSL 428
QY 451 RPNATYSVCVMP 462
DB 429 RAIQTLLHAQNP 440

RESULT 7
A:Title: oncofetal trophoblast glycoprotein 5T4 precursor - human
N:Alternate names: oncofetal antigen 5T4
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A53531; S40087
R:Myers, K.A.; Rahi-Saund, V.; Davison, M.D.; Young, J.A.; Cheater, A.J.; Stern, P.L.
J. Biol. Chem. 269, 9319-9324, 1994
A:Title: Isolation of a cDNA encoding 5T4 oncofetal trophoblast glycoprotein. An antigen
A:Reference number: A53531; MUID:94179356; PMID:8132670
A:Accession: A53531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-420 <ME>
A:Cross-references: UNIPROT:Q13641; UNIPARC:UPI000004CAD5; EMBL:Z29083; NID:9435654; PID
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-420/Product: oncofetal trophoblast glycoprotein 5T4 #status predicted <MAT>

Query Match 8.4%; Score 264.5; DB 2; Length 420;
Best Local Similarity 28.1%; Pred. No. 2.9e-08;
Matches 103; Conservative 44; Mismatches 121; Indels 99; Gaps 15;

QY 2 CSRVP-----LLLPLLLLLALG-----PGVQCPS 26
DB 5 CSRGPAAGDGLRLARLALVLLGWSSSPTSSASSFSSAPFLASAVSAQPLPDQCPA 64
QY 27 GCQCQSQ-POTVFTCTARQGTTPRDPVPPDVTGLYVFNENGITMLDASSFAGLP---GLQLLD 82
DB 65 LCECSEARTVKVRNRLTEVPTDLPAYVRNLFLTGNQLAVLPAGAFARPPPLAELALN 124
QY 83 LSONQIASLR-----LPRLLLDLSHNSLLALEPGILDTANVEALRLAGLGLQLDEGL 136

DB 125 LSGSRLDEVRAGAEHLPSLRQLDLSHNPLADLSPPAFSGSNASV-----SAPSPL 175
QY 137 FSLRLNHLDDVSDNQLER-----VPPVI--RGLRGLRLRAGNTRIAQLRPEDLAGL 188
DB 176 VEILN-HIYPPDEDERQNRSEFGVVAALLAGRALQGLRLLELASN-HFLYLRDVLQAOL 233
QY 189 AALQELDVSNLSLQALP-----GDLGLFPRLRLLAA 220
DB 234 PSLEHLDLSSNSLSVSLTYVSFRNLTHLESIAHLEDNALKVLHNGTFLAELQGL-PHIRVF-L 291
QY 221 ARNPFNCVPLSWFGPWRSHVTLASPEETRCHPPKPNAGRLLELDYADFGC-----PA 276
DB 292 DNNPWCDCMADVMVTLKETEV-VQGRDLTICAYPEKMRNRVILNELNSADLDCDPILPP 350
QY 277 TTTTATV 283
DB 351 SLOTSYV 357

RESULT 8
A:Title: MEGF5 protein - rat
N:Alternate names: slit protein homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13953
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13953
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1523 <NAK>
A:Cross-references: UNIPROT:O88280; UNIPARC:UPI000000ESF7A; EMBL:AB011531; NID:93449291; I
C:Genetics:
A:Gene: MEGF5
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein re

Query Match 8.3%; Score 261; DB 2; Length 1523;
Best Local Similarity 26.3%; Pred. No. 2e-07;
Matches 93; Conservative 41; Mismatches 126; Indels 94; Gaps 14;

QY 24 CPSCQCQSQPTVCTARQGTTPRDPVPPDVTGLYVFNENGITMLDASSFAGLPGQLQLDL 83
DB 725 CPEQCTCVE-TVVRCSNRGLHTLPGMKVDVTELYLSEGNHLYAV----- 767
QY 84 SONQIASLRPLRLLLDLSHNSLLALEPGILDTANVEALRLAGLGLQLDEGLFSRLRLN 143
DB 768 -PKELSTFR--QLTLIDLSSNS-----ISMLTNHTFSNNSHL 801
QY 144 HDLDVSDNQLERVP-PVIRGLRGLRLRAGNTRIAQLRPEDLAGLALQELDVSNLSLQ 202
DB 802 STLILSYNRLRCIPVHAFNGLSRLVLTLCGN-----DISSVPEGSFNLTLSL-- 850
QY 203 ALPGDLGLFPRLLILAAARNPFCVPLSWFGPWRSHVTLASPEETRCHPPKPNAGR 262
DB 851 -----HLALGINPLHCDCSLRSLWSEWIKAGY---KEPGIARCSSPESMADR 893
QY 263 LLELDYADFGCPATTTTATVTPTRPVVREPTALSSSLAPTTLWLSPTAPATEAPSPSTAP 322
DB 894 LLLTTPTRHFOCKG-----PVDINIVAKNACLSS--PCKNNGTCSQDPVEQVRCYTCP 944
QY 323 PTVGVPQPOQC--PPSTCL-----NGTCHLGRHH--LACLCPEGFTGLYCE 367
DB 945 YSY-----KGKDTVPINTCVQNQCQHGCTCHLSESHRDGFCSCPLGPEGORCE 994

RESULT 9
B36665
A:Title: slit protein 2 precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C;Accession: B36665
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and co
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: B36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1469 <ROT>
A;Cross-references: UNIPARC:UPI0000177454; GB:X53959
C;Genetics:
A;Gene: FlyBase:gli
A;Cross-references: FlyBase:FBgn0003425
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein x
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: proteoglycan amino-terminal homology <PAH5>
F;1068-1099/Domain: EGF homology <EGF>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1469;
Best Local Similarity 21.4%; Pred. No. 3.9e-07;
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;
QY 24 CPSCQCSQQTVECTARQGTTPRDVP-----PDTGLY 58
DB 519 CPAMCHC-EGTVDCTGRRUKKEIPDIPLHTTELLLDNDELGRITSSDGLFRLPHLYKLE 577
QY 59 VFENGITMLDASSPAGLPGLQLLDLSNQIAS-----LRLPRLLLDLGHNSLLALEPG 112
DB 578 LKRNQLTGIEPNAPEGASHIQELQGENKKEISNKNMFLGHLQKLTNLVDNQISCVWPG 637
QY 113 ILDTAN-----VEALRLAGLQQLQDEGLFSLRLNRLHDLVD--- 148
DB 638 SFEHLNLSLTSLNLASPNFNCNCHLAWFAECVRKSLNGGAARCGAPSKVRDQVKDLPHS 697
QY 149 -----SDQLERVP-----PV----- 159
DB 698 EFKCSSNSEGLGDGYCPSCCTGTGTVACSRNQLKEIPRGIPAEITSLEYLSNEIEQI 757
QY 160 ----IRGLGLTRLRAGNTRIAQLRPEDLAGLAALQELDVS-----NL 199
DB 758 HYERIRHLRSITRLDLS-NNQITILSNYTFANLTLSLISYNKLOCLQRHALSGLNLL 816
QY 200 SLQALPGDLGSLFPR-----LRLAAARNPNCVCPISWFGPWWVRESHVTLASPEET 251
DB 817 RVVSLHGNRISMLPEGSFEDLKS LTHIALGNSPLYCDGLKWFSDWKLDV---EPGIA 873
QY 252 RCHFPKNAERLLLELDYADGCGPATTTATVTPTRVPRVREPTALSSSLAFTWLSPTAPA 311
DB 874 RCAEPQMKDKLILSTPSSSFVCRGRVRNRDILAKNCNCFEQPCQNOQCQV-----ALPQ 927

QY 312 TEAPSPPESTAPPTVGPVPQP-----QDCPPSTCLNGGTCHLGTTRHHLACLPEPG 360
DB 928 REYQC-----LCQPGYHKHCKEFMIDACVGNPCRNATCTVLEEGRFSCQCAPG 976
QY 361 FTGLYCESQM 370
DB 977 YTGARCTNI 986

RESULT 10

A36665
slit protein 1 precursor - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 02-Aug-2002
C;Accession: A36665; A31640; S13523
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A;Title: slit: an extracellular protein necessary for development of midline glia and co
A;Reference number: A36665; MUID:91099665; PMID:2176636
A;Accession: A36665
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1480 <ROT>
A;Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A;Title: slit: An EGF-homologous locus of *D. melanogaster* involved in the development of
A;Reference number: A31640; MUID:89077533; PMID:3144436
A;Accession: A31640
A;Molecule type: DNA
A;Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', 'RO2'
A;Cross-references: UNIPARC:UPI000016BD7A; GB:M23543; NID:9340939; PID:9514357
C;Genetics:
A;Gene: FlyBase:gli
A;Cross-references: FlyBase:FBgn0003425
A;Introns: 1351/3
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein x
C;Keywords: alternative splicing; growth factor
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F;791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F;815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F;1028-1061/Domain: EGF homology <EGF>
F;1068-1099/Domain: EGF homology <EGF2>
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1480;
Best Local Similarity 21.4%; Pred. No. 4e-07;
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;

Db 123 LEENKLTPEKCLYGLSLQELVYVHNLSSAISFGAFVGLHLLRLHLNLSRLQMINSK 182

Qy 115 ---DTANVEALRL-----AGLGLQQLDEGLFRLRLNLHDL 147

Db 183 WFEALPNLEILMLGDNPIRLKDMNFQPLLKRLRSVIAGINLVEPDDALVLENLESIS 242

Qy 148 VSDNQLERP-----PVIRGLRG----- 165

Db 243 FYDNRLNKVPOVALQKAVNLKFLDLNKNPILNIRRGDFSNMHLKELGINNPELVSDS 302

Qy 166 -----LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSLQAL-PGDSGLGFRLR 216

Db 303 LAVDNLPDLRKIEATNNPRLSVIHPNAPFRPKLESMLNSNLSALVHGIESL-PNLK 361

Qy 217 LLAARNPNCVCPISFGPWVRSHVTLASPEETRCHFPKKNAGRLLELDYADFGCPA 276

Db 362 EISHSNPIRDCVIRWIN--MNKTINIRFMEPDSLFCVDPPEFQCNVRQVHFRDM---- 415

Qy 277 TTTTATVPTTRPVVREPTALSSSL---APTWLSPTAPATEAPSPSTAPPTVGVPPQPD 333

Db 416 -----MEICUPLI-APESFPSILDVEADSVSLHCRATAEPQ-----PRIYWTSPGKR 463

Qy 334 CPPSTCLNGGTCHL-GTRHHLACLCEGFTGLY---CESOMGQGRPSPTPVTPRPPR-- 387

Db 464 LLPNTLREKFVHSEGTDIRGITPEKG--GLYTCTIATNLVGADLKSIMIKVGGFVQDN 521

Qy 388 --SLTLGTEPVSPTSLRVLQRYLQGSVQLRSRLTYRNLSPDKRLVTLRLPASLAEY 445

Db 522 NGSNLKIRDIRANSVLVS---WKANSKILKSSVKWTAFTVKTEDSQAAQSARIPSDVKVY 578

Qy 446 TVTQLRPNATYSVCV 460

Db 579 NLTHLKPSTEXKICI 593

RESULT 15

T42626

secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)

N:Alternate names: neurogenic extracellular slit protein

C:Species: Mus musculus (house mouse)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42626

R:Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H. Mech. Dev. 79, 57-72, 1998

A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in

A:Reference number: 222177; MUID:99279238; PMID:10349621

A:Accession: T42626

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1025 <HOL>

A:Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI00000E8104; EMBL:AF074960; NID:g4151258;

C:Genetics:

A:Gene: Slit2

C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein 1

Query Match 7.4%; Score 231; DB 2; Length 1025;

Best Local Similarity 24.0%; Pred. No. 6.9e-06;

Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;

Qy 24 CPSGCCSQPQTVFCTARQGTTPRDPVDPDTVGLVVFENGITMLDASSFAGLPGQLLDL 83

Db 223 CPSECTCLD-TXVRCNKGKLVLPKIPKDVTELYDGNQFTLV--PKELSNYKHLTLIDL 280

Qy 84 SONQIASL-----RLPRLLLDLSHNSLLALEPGILDITANVEALRLAGLGLQQLDEGLF 137

Db 281 SNNRISTLSNQXFSNMTQLTLILSNRLRCIPRPTD-----GLKSL----- 323

Qy 138 SRLRLNHLDVDNQLERVPVIRGLRLRLAGNTRIAQLRPEDLAGLAALQELDVS 197

Db 324 -RLLSLHGNDIS-----VVP----- 337

Qy 198 NLSLQALPGDLSGLPRLRLAAARNPFCVPLSWFGFPVWRESHVTLASPEETRCHFP 257

Db 338 -----EGAFNDLSA-----LSHLAIGANPLYCDNCNQWLSDMVKSEY---KEPGIARCAGPG 386

Qy 258 KNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP 317

Db 387 EMADKLLLTTPSKKFTCQ-----GPMDDITIOAKCNPCLSN 421

Qy 318 PSTAPPTVGPVP-----QPQDCP-----PSTCLNGGTCHL--GTRHHLACL 356

Db 422 PCKNDGTCNNNDPVDVDFYRCTCPYGFQGDQDVPFHACISNPKHGCTCHLKEGENAGFWCT 481

Qy 357 CPEGFTGLYCE 367

Db 482 CADGFEENCE 492

Search completed: January 5, 2006, 13:54:15

Job time : 43 secs

105	1534	2	Q5VW17_HUMAN	8.6	270	Q5VW17 homo sapien	178	242.5	7.7	545	1	CPN2_HUMAN	P22792 homo sapien
106	409	2	Q5T0V2_HUMAN	8.6	268.5	Q5T0V2 homo sapien	179	242.5	7.7	718	2	O6PCK4_XENLA	O6PCK4 xenopus lae
107	417	2	Q8E4U7_PETMA	8.5	268	Q8E4J7 petromyzon	180	242	7.7	380	2	Q5TUV3_HUMAN	Q5TUV3 homo sapien
108	1512	2	Q9DE36_BRARE	8.5	267.5	Q9DE36 brachydanio	181	242	7.7	652	2	Q7PV23_ANOGA	Q7PV23 anopheles g
109	1529	2	Q7ZX12_XENLA	8.5	266.5	Q7ZX12 xenopus lae	182	241.5	7.7	272	2	O4KPI2_LAMAP	O4KPI2 lampetra ap
110	460	2	Q6IPI6_HUMAN	8.5	266	Q6IPI6 homo sapien	183	241.5	7.7	311	2	O6E4L3_PETMA	O6E4L3 petromyzon
111	734	2	Q35930_MOUSE	8.5	266	Q35930 mus musculus	184	240	7.7	560	1	GPV_HUMAN	P40197 homo sapien
112	1044	2	Q3IS89_MACFA	8.5	265.5	Q3IS89 macaca fasc	185	239.5	7.6	370	2	O8BGX3_MOUSE	O8BGX3 m mus muscu
113	298	2	Q4GIL7_EPTBU	8.5	265	Q4GIL7 eptatretus	186	239.5	7.6	786	2	Q5TU01_ANOGA	Q5TU01 anopheles g
114	734	2	Q5SX47_MOUSE	8.4	265	Q5SX47 mus musculus	187	239.5	7.6	1256	2	Q7QC72_ANOGA	Q7QC72 anopheles g
115	420	1	TPBG_HUMAN	8.4	264.5	Q13641 homo sapien	188	238	7.6	323	2	O4KPI3_9PETR	O4KPI3 ichtthyomyzo
116	334	2	Q5VSG2_HUMAN	8.4	264	Q5VSG2 homo sapien	189	238	7.6	453	2	O86XV1_HUMAN	O86XV1 homo sapien
117	352	2	Q4G1L1_EPTBU	8.4	264	Q4G1L1 eptatretus	190	238	7.6	544	2	O8UV23_9PERC	O8UV23 spherooides
118	332	2	Q5I0E1_RAT	8.4	263	Q5I0E1 rattus norv	191	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9D3K0 m mus muscu
119	1253	2	Q4T0S1_TETNG	8.4	263	Q4T0S1 tetraodon n	192	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4S4C0 tetraodon n
120	346	2	Q4G1L9_EPTBU	8.4	262	Q4G1L9 eptatretus	193	237	7.6	289	2	O4KP06_LAMAP	O4KP06 lampetra ap
121	347	1	A2GL3_HUMAN	8.3	261.5	P02750 homo sapien	194	237	7.6	370	2	O8N967_HUMAN	O8N967 homo sapien
122	1523	1	SLIT3_RAT	8.3	261	O8B280 rattus norv	195	237	7.6	578	1	LRC15_RAT	O8R5M3 rattus norv
123	321	2	Q6E4D1_PETMA	8.2	258	Q6E4D1 petromyzon	196	237	7.6	707	2	Q9ESV6_RAT	Q9ESV6 rattus norv
124	1523	1	SLIT3_HUMAN	8.2	258	Q75094 homo sapien	197	237	7.6	1046	2	Q7P217_ANOGA	Q7P217 anopheles g
125	324	2	Q4S3K9_TETNG	8.2	257.5	Q4S3K9 tetraodon n	198	236.5	7.5	461	2	Q4SAL2_TETNG	Q4SAL2 tetraodon n
126	501	2	Q4SZC5_TETNG	8.2	257.5	Q4SZC5 tetraodon n	199	236.5	7.5	715	2	O4RY04_TETNG	O4RY04 tetraodon n
127	473	1	RTN4R_RAT	8.2	257	Q89M75 rattus norv	200	236	7.5	707	2	Q8CBC6_MOUSE	Q8CBC6 mus musculus
128	739	2	Q8BKX5_MOUSE	8.2	257	Q8BKX5 mus musculus	201	236	7.5	718	2	O6P6Z7_XENLA	O6P6Z7 xenopus lae
129	342	2	Q4SGG5_TETNG	8.2	256.5	Q4SGG5 tetraodon n	202	235.5	7.5	296	2	O4G1H6_EPTST	O4G1H6 eptatretus
130	1095	2	Q90XG4_CHICK	8.1	255.5	Q90XG4 gallus gall	203	235.5	7.5	579	1	LRC15_MOUSE	O80X72 mus musculus
131	528	2	Q8N644_HUMAN	8.1	254	Q8N644 homo sapien	204	235	7.5	574	2	Q4RRR5_TETNG	Q4RRR5 tetraodon n
132	1523	1	SLIT3_MOUSE	8.1	254	Q9WVB4 mus musculus	205	234.5	7.5	488	2	Q4RK86_TETNG	Q4RK86 tetraodon n
133	311	2	Q6E4L1_PETMA	8.0	253	Q6E4L1 petromyzon	211	231.5	7.4	283	2	O4G1H4_EPTST	Q4G1H4 eptatretus
134	426	1	TPBG_RAT	8.0	252	Q9QV5 rattus norv	212	231.5	7.4	840	1	SLIK6_MOUSE	O8C110 mus musculus
140	567	2	Q9QZU3_MOUSE	8.0	252	Q9QZU3 mus musculus	213	231	7.4	294	2	O5VT99_HUMAN	O5VT99 homo sapien
141	473	1	RTN4R_MOUSE	8.0	252	Q9ZPQ3 mus musculus	214	231	7.4	547	1	CPN2_MOUSE	O9DBB9 mus musculus
142	542	2	Q9N4G6_CABEL	8.0	251	Q9ZPI8 mus musculus	215	231	7.4	619	2	Q7QBW2_ANOGA	Q7QBW2 anopheles g
143	622	2	Q9ZW15_HUMAN	8.0	251	Q9N4G6 caenorhabdi	216	231	7.4	707	2	O642B4_RAT	Q642E4 rattus norv
144	622	2	Q7Z2Q7_HUMAN	8.0	251	Q6ZW15 homo sapien	217	231	7.4	787	2	O4SW26_TETNG	Q4SW26 tetraodon n
145	1021	2	Q9V430_DROME	8.0	251	Q7Z2Q7 homo sapien	218	230.5	7.4	687	2	O4SCX3_TETNG	Q4SCX3 tetraodon n
146	412	2	Q4RRU8_TETNG	8.0	250	Q9V430 drosophila	219	230	7.3	332	2	O8QFN6_ELAQU	O8QFN6 elaphe quad
147	412	2	Q4RRU8_TETNG	8.0	250	Q4RRU8 tetraodon n	220	230	7.3	332	2	O8QFN7_ELAQU	O8QFN7 elaphe quad
148	789	1	LRFN2_HUMAN	8.0	249.5	Q9ULH4 homo sapien	221	230	7.3	872	2	O4SZ04_TETNG	Q4SZ04 tetraodon n
149	2597	2	Q6WRH9_RAT	8.0	249.5	Q9BE71 macaca fasc	222	230	7.3	1229	2	Q4T7S0_TETNG	Q4T7S0 tetraodon n
150	420	1	TPBG_MACFA	7.9	248.5	Q9WRH9 rattus norv	223	229.5	7.3	828	2	O8C8T7_MOUSE	Q8C8T7 mus musculus
151	481	1	NYX_HUMAN	7.9	248	Q4R8Y9 macaca fasc	224	229	7.3	581	1	LRC15_HUMAN	O8TF66 homo sapien
152	305	2	Q5H983_HUMAN	7.9	248	Q9GZU5 homo sapien	225	228.5	7.3	294	2	O6ZSA7_PETMA	O6ZSA7 petromyzon
153	481	2	Q5H983_HUMAN	7.9	248	Q5H983 homo sapien	226	228.5	7.3	341	2	O6ZSA7_HUMAN	O6ZSA7 homo sapien
154	305	2	Q5H983_HUMAN	7.9	247.5	Q4G1L3 eptatretus	227	228.5	7.3	342	2	O4RRU5_TETNG	Q4RRU5 tetraodon n
155	1521	1	SLIT2_MOUSE	7.9	247.5	Q4G1L3 eptatretus	228	228	7.3	310	2	Q4RRU4_TETNG	Q4RRU4 tetraodon n
156	1529	1	SLIT2_HUMAN	7.9	247.5	Q9R1B9 mus musculus	229	228	7.3	388	2	O4SPP9_TETNG	Q4SPP9 tetraodon n
157	794	2	Q90W23_XENLA	7.9	247.5	Q90W23 xenopus lae	230	227.5	7.3	356	2	O8BXQ3_MOUSE	Q8BXQ3 m mus muscu
158	308	2	Q4SK16_TETNG	7.9	247	Q4SK16 tetraodon n	231	227	7.2	326	2	O4KLI3_RAT	Q4KLI3 rattus norv
159	246	2	Q4G1L3_EPTST	7.8	246	Q4G1L3 eptatretus	232	227	7.2	783	2	O90XG2_CHICK	O90XG2 gallus gall
160	331	2	Q91W20_MOUSE	7.8	245.5	Q91W20 mus musculus	233	227	7.2	950	2	O90Z44_CHICK	O90Z44 gallus gall
161	544	2	Q61X58_CABER	7.8	245.5	Q61X58 caenorhabdi	234	226.5	7.2	283	2	O4G1L1_EPTST	O4G1L1 eptatretus
162	306	2	Q4G1K6_EPTST	7.8	245	Q4G1K6 eptatretus	235	226.5	7.2	298	2	O4KPI5_9PETR	O4KPI5 ichtthyomyzo
163	321	2	Q6E4U9_PETMA	7.8	245	Q6E4J9 petromyzon	236	226.5	7.2	299	2	O4G1I9_EPTST	Q4G1I9 eptatretus
164	708	2	Q8IYQ6_HUMAN	7.8	245	Q8IYQ6 homo sapien	237	226.5	7.2	557	1	LG11_HUMAN	O95970 homo sapien
165	245	2	Q5R482_PONPY	7.8	245	Q5R482 pongo pygma	238	226.5	7.2	719	1	LRFN5_HUMAN	O96N16 homo sapien
166	411	2	Q4S616_TETNG	7.8	244.5	Q4S616 tetraodon n	239	226	7.2	321	2	O4KP16_9PETR	O4KP16 ichtthyomyzo
167	718	2	Q73675_XENLA	7.8	244.5	Q73675 xenopus lae	240	226	7.2	364	2	O4SQ63_TETNG	Q4SQ63 tetraodon n
168	766	1	SLIT2_RAT	7.8	244.5	Q9WVC1 rattus norv	241	225.5	7.2	210	2	O4SCF1_TETNG	Q4SCF1 tetraodon n
169	788	1	LRFN2_MOUSE	7.8	244.5	Q80TG9 mus musculus	242	225.5	7.2	298	2	O6E4J3_PETMA	O6E4J3 petromyzon
170	1593	2	Q5DTL5_MOUSE	7.8	244.5	Q5DTL5 mus musculus	243	223.5	7.1	283	2	O4G1H8_EPTST	O4G1H8 eptatretus
171	458	2	Q6WZD3_BRARE	7.8	244	Q6WZD3 brachydanio	244	223.5	7.1	647	2	O4S1N0_TETNG	O4S1N0 tetraodon n
172	567	1	GPV_RAT	7.8	244	O8770 rattus norv	245	223	7.1	289	2	O6E4C8_PETMA	O6E4C8 petromyzon
173	708	2	Q9H3W5_HUMAN	7.8	244	Q9H3W5 homo sapien	246	223	7.1	349	2	O4SH52_TETNG	Q4SH52 tetraodon n
174	476	1	NYX_MOUSE	7.8	243.5	P83503 mus musculus	247	222.5	7.1	413	2	O642I5_MOUSE	O642I5 mus musculus
175	321	2	Q6E4L4_PETMA	7.8	243	Q6E4L4 petromyzon	248	222.5	7.1	557	1	LG11_RAT	O8K4Y5 rattus norv
176	708	2	Q6I9V8_HUMAN	7.8	243	Q6I9V8 homo sapien	249	222.5	7.1	557	2	O5R945_PONPY	O5R945 pongo pygma
177	388	2	Q6ZM54_BRARE	7.7	242.5	Q6ZM54 brachydanio	250	222.5	7.1	557	2	O5FWS7_RAT	Q5FWS7 rattus norv

251	222.5	7.1	792	2	Q90Z43	CHICK
252	222	7.1	269	2	Q6E4J0	PETMA
253	222	7.1	348	2	Q95JU8	WACFA
254	222	7.1	722	2	Q5PU22	XENIA
255	221.5	7.1	475	2	Q4T109	TETNG
256	221.5	7.1	557	1	LG11	MOUSE
257	221.5	7.1	719	1	LRFN5	MOUSE
258	221.5	7.1	721	2	Q5DTH4	MOUSE
259	221	7.0	1093	1	LRIG1	HUMAN
260	220.5	7.0	210	2	Q6E4M1	PETMA
261	220.5	7.0	306	2	Q4KP04	LAMPAP
262	220.5	7.0	322	2	Q6E4K1	PETMA
263	220.5	7.0	342	2	Q4R894	TETNG
264	220.5	7.0	342	2	LRTM2	MOUSE
265	220.5	7.0	515	1	Q8CB1U	MOUSE
266	220.5	7.0	733	2	Q24250	DRONE
267	220.5	7.0	841	1	SLIK6	HUMAN
268	220	7.0	582	1	LRTB31	MOUSE
269	220	7.0	582	2	Q8BZA0	MOUSE
270	220	7.0	603	2	Q4S027	TETNG
271	219.7	7.0	583	2	Q4SNQ0	TETNG
272	219	7.0	334	2	Q6P7C4	RAT
273	218.5	7.0	359	2	Q6GTU0	HUMAN
274	218.5	7.0	618	1	LRC21	MOUSE
275	217.5	6.9	288	2	Q8BR15	MOUSE
276	217.5	6.9	615	2	Q4SLS7	TETNG
277	217.5	6.9	695	2	Q4TIY8	TETNG
278	217.5	6.9	1335	2	Q610C7	CAEBR
279	217	6.9	637	2	Q6DCV7	XENIA
280	216	6.9	263	2	Q6E4C7	PETMA
281	216	6.9	282	2	Q4GL16	EPTST
282	216	6.9	514	2	Q4VBX1	MOUSE
283	215.5	6.9	329	2	Q56NG5	CIOIN
284	215.5	6.9	331	1	PLIB	AGBL
285	215.5	6.9	612	2	Q4SVK9	TETNG
286	215.5	6.9	737	2	Q9VU51	DRONE
287	215	6.9	743	2	Q6P1M7	HUMAN
288	214.5	6.8	329	2	Q56NG6	CIOIN
289	214.5	6.8	441	2	Q86UN2	HUMAN
290	214.5	6.8	716	1	LRRN1	HUMAN
291	214.5	6.8	731	2	Q4T145	TETNG
292	214.5	6.8	1535	2	Q23991	DRONE
293	214	6.8	295	2	Q6E4C9	PETMA
294	214	6.8	516	1	LRTM2	HUMAN
295	214	6.8	717	2	Q4SR34	TETNG
296	214	6.8	2828	2	Q9NR39	HUMAN
297	213.5	6.8	238	2	Q6E4J5	PETMA
298	213.5	6.8	273	2	Q4GL12	EPTBU
299	213.5	6.8	359	1	CHAD	HUMAN
300	213.5	6.8	361	1	CHAD	BOVIN
301	213	6.8	438	2	Q7TQ96	RAT
302	213	6.8	716	1	LRRN1	MOUSE
303	212.5	6.8	604	2	Q4SHE8	TETNG
304	212	6.8	276	2	Q4GLJ9	EPTST
305	212	6.8	445	2	Q80WD0	RAT
306	212	6.8	918	2	Q7Q3F0	ANOCA
307	211.5	6.7	192	2	Q6E4I9	PETMA
308	211.5	6.7	270	2	Q6E4I7	PETMA
309	211.5	6.7	518	2	Q5R712	PONPY
310	211	6.7	187	2	Q6E4I2	PETMA
311	211	6.7	581	1	LRTM3	HUMAN
312	211	6.7	581	1	LRTM3	EPTBU
313	210.5	6.7	257	2	Q4GIM3	PETMA
314	210.5	6.7	321	2	Q6E4I5	PETMA
315	210.5	6.7	4303	1	PKD1	HUMAN
316	210	6.7	358	1	CHAD	RAT
317	210	6.7	1028	2	Q6E5R7	PIG
318	209.5	6.7	214	2	Q6E4H0	PETMA
319	209.5	6.7	533	2	Q5E9T6	BOVIN
320	209	6.7	211	2	Q6E4I3	PETMA
321	209	6.7	257	2	Q6E4J6	PETMA
322	209	6.7	353	2	Q6UXX1	HUMAN
323	209	6.7	358	1	CHAD	MOUSE

324	209	6.7	358	2	Q5UV4_MOUSE	Q5UV4_MOUSE
325	209	6.7	391	2	Q4SB7_TETNG	Q4SB7_TETNG
326	209	6.7	1091	1	LRIG1_MOUSE	LRIG1_MOUSE
327	208.5	6.7	350	2	Q5RH06_BRARE	Q5RH06_BRARE
328	208.5	6.7	382	1	PRELP_HUMAN	PRELP_HUMAN
329	208.5	6.7	382	2	Q6PHG6_HUMAN	Q6PHG6_HUMAN
330	208.5	6.7	382	2	Q6FG38_HUMAN	Q6FG38_HUMAN
331	208.5	6.7	445	2	Q8K0S5_MOUSE	Q8K0S5_MOUSE
332	208.5	6.7	479	2	Q6X3Y5_BRARE	Q6X3Y5_BRARE
333	208.5	6.7	518	1	LRTW4_HUMAN	LRTW4_HUMAN
334	208.5	6.7	518	2	Q4F298_HUMAN	Q4F298_HUMAN
335	208.5	6.7	519	2	Q4KWX1_HUMAN	Q4KWX1_HUMAN
336	208.5	6.7	537	1	LG14_HUMAN	LG14_HUMAN
337	208.5	6.7	590	2	Q6VXJ7_HUMAN	Q6VXJ7_HUMAN
338	208	6.6	649	2	Q9VXK22_DROME	Q9VXK22_DROME
339	207.5	6.6	180	2	Q6BA4F0_PETMA	Q6BA4F0_PETMA
340	207.5	6.6	330	2	Q4S074_TETNG	Q4S074_TETNG
341	207.5	6.6	518	2	Q6Z731_HUMAN	Q6Z731_HUMAN
342	207.5	6.6	1329	1	GP124_MOUSE	GP124_MOUSE
343	207	6.6	313	2	Q5T9K5_HUMAN	Q5T9K5_HUMAN
344	207	6.6	313	2	Q8N7C0_HUMAN	Q8N7C0_HUMAN
345	207	6.6	536	2	Q6P0D2_BRARE	Q6P0D2_BRARE
346	207	6.6	613	2	Q50144_CHICK	Q50144_CHICK
347	207	6.6	740	2	Q5JNV6_HUMAN	Q5JNV6_HUMAN
348	207	6.6	4293	2	Q08852_MOUSE	Q08852_MOUSE
349	206.5	6.6	270	2	Q6BAK6_PETMA	Q6BAK6_PETMA
350	206.5	6.6	274	2	Q6BAC1_PETMA	Q6BAC1_PETMA
351	206.5	6.6	274	2	Q6BAI2_PETMA	Q6BAI2_PETMA
352	206.5	6.6	294	2	Q5U4S7_XENLA	Q5U4S7_XENLA
353	206.5	6.6	327	2	Q5U4S7_XENLA	Q5U4S7_XENLA
354	206.5	6.6	423	2	Q8ND46_HUMAN	Q8ND46_HUMAN
355	206.5	6.6	614	2	Q9D1T0_MOUSE	Q9D1T0_MOUSE
356	206	6.6	353	2	Q9UJX9_HUMAN	Q9UJX9_HUMAN
357	206	6.6	353	2	Q8WUA8_HUMAN	Q8WUA8_HUMAN
358	206	6.6	381	1	PRELP_BOVIN	PRELP_BOVIN
359	206	6.6	428	2	Q14498_HUMAN	Q14498_HUMAN
360	206	6.6	539	2	Q5TPW2_ANOGA	Q5TPW2_ANOGA
361	206	6.6	606	2	Q8BZD4_MOUSE	Q8BZD4_MOUSE
362	206	6.6	606	2	Q8BLC0_MOUSE	Q8BLC0_MOUSE
363	206	6.6	738	1	Q5UIA7_DROME	Q5UIA7_DROME
364	206	6.6	1054	1	LRIG2_MOUSE	LRIG2_MOUSE
365	206	6.6	1127	2	Q4TAT9_TETNG	Q4TAT9_TETNG
366	205.5	6.6	212	2	Q6B4H2_PETMA	Q6B4H2_PETMA
367	205.5	6.6	479	2	Q6DH76_BRARE	Q6DH76_BRARE
368	205.5	6.6	492	2	Q99XT6_MOUSE	Q99XT6_MOUSE
369	205.5	6.6	590	1	LRTW4_MOUSE	LRTW4_MOUSE
370	205	6.5	248	2	Q4G1K3_EPTST	Q4G1K3_EPTST
371	205	6.5	256	2	Q4GLL6_EPTBU	Q4GLL6_EPTBU
372	205	6.5	486	2	Q4RU74_TETNG	Q4RU74_TETNG
373	205	6.5	614	2	Q5RDJ4_PONPY	Q5RDJ4_PONPY
374	205	6.5	614	2	Q9N008_MACFA	Q9N008_MACFA
375	205	6.5	620	2	Q9GFE5_HUMAN	Q9GFE5_HUMAN
376	205	6.5	740	1	CT075_HUMAN	CT075_HUMAN
377	204.5	6.5	463	2	Q8CLV9_MOUSE	Q8CLV9_MOUSE
378	204	6.5	353	2	Q6QMY6_RAT	Q6QMY6_RAT
379	204	6.5	1173	2	Q9VJ78_DROME	Q9VJ78_DROME
380	204	6.5	1306	2	Q6P4S1_XENLA	Q6P4S1_XENLA
381	203.5	6.5	845	2	Q6AI13_HUMAN	Q6AI13_HUMAN
382	203.5	6.5	894	2	Q9VKG3_DROME	Q9VKG3_DROME
383	203.5	6.5	1061	2	Q53ME4_HUMAN	Q53ME4_HUMAN
384	203.5	6.5	1065	1	LRIG2_DROME	LRIG2_DROME
385	203	6.5	269	2	Q6B4B6_PETMA	Q6B4B6_PETMA
386	203	6.5	428	2	Q5NVQ6_PONPY	Q5NVQ6_PONPY
387	203	6.5	602	2	Q4R3P6_MACFA	Q4R3P6_MACFA
388	203	6.5	703	2	Q4SLZ4_TETNG	Q4SLZ4_TETNG
389	203	6.5	1514	2	Q6NN49_DROME	Q6NN49_DROME
390	203	6.5	1514	2	Q9NBK9_DROME	Q9NBK9_DROME
391	203	6.5	1514	2	Q9VUN0_DROME	Q9VUN0_DROME
392	202.5	6.5	259	2	Q4G1K1_EPTST	Q4G1K1_EPTST
393	202.5	6.5	259	2	Q4G1H5_EPTST	Q4G1H5_EPTST
394	202.5	6.5	274	2	Q6B4J2_PETMA	Q6B4J2_PETMYZON
395	202.5	6.5	829	2	Q4RIG0_TETNG	Q4RIG0_TETNG
396	202	6.4	271	2	Q4KPI1_LAMAP	Q4KPI1_LAMPETRA AP

397	202	6.4	1117	2	Q5VQM7	ORYZA	Q5vqm7	oryza sativ	470	194	6.2	692	2	Q4RV46	TETNG	Q4rv46	tetraodon n
398	201.5	6.4	187	2	Q6E4D7	PETMA	Q6e4d7	petromyzon	471	194	6.2	836	2	Q9V9V6	DROME	Q9v9v6	drosophila
399	201.5	6.4	275	2	Q4G1J5	EPTST	Q4g1j5	epitretus	472	193.5	6.2	186	2	Q6E4H8	PETMA	Q6e4h8	petromyzon
400	201.5	6.4	372	2	Q8CBR6	MOUSE	Q8cbr6	mus musculus	473	193.5	6.2	270	2	Q4KP03	LAMAP	Q4kp03	lampetra ap
401	201.5	6.4	457	2	Q4G0D1	DROSOPHILA	Q4g0d1	drosophila	474	193.5	6.2	373	1	Q4G1M1	EPTTB	Q4g1m1	epitretus
402	201.5	6.4	524	2	Q9G5D9	TETNG	Q9g5d9	tetraodon n	475	193.5	6.2	277	1	PRELP	RAT	PRELP	rattus norv
403	201.5	6.4	551	2	Q4RF95	TETNG	Q4rf95	tetraodon n	476	193.5	6.2	378	2	Q8CAZ9	MOUSE	Q8caz9	mus musculus
404	201.5	6.4	606	2	Q9BZ20	HUMAN	Q9bzz20	homo sapien	477	193.5	6.2	421	2	Q9NT99	HUMAN	Q9nt99	homo sapien
405	201.5	6.4	892	2	P91644	DROSOPHILA	P91644	drosophila	478	193.5	6.2	423	2	Q6IDG7	DROME	Q6idg7	drosophila
406	201.5	6.4	1527	2	Q9VZZ4	DROSOPHILA	Q9vzz4	drosophila	479	193.5	6.2	545	1	LG12	HUMAN	LG12	homo sapien
407	201	6.4	213	2	Q6E4H6	PETMA	Q6e4h6	petromyzon	480	193.5	6.2	574	2	Q6OWE8	CAEBR	Q6owe8	caenorhabdi
408	201	6.4	218	2	Q6E4K9	PETMA	Q6e4k9	petromyzon	481	193.5	6.2	721	1	Y2082	MYCTU	Y2082	mycobacteri
409	201	6.4	336	2	Q4S8M5	TETNG	Q4s8m5	tetraodon n	482	193.5	6.2	721	2	Q7TZ24	MYCBO	Q7tz24	mycobacteri
410	201	6.4	354	2	Q4W655	MOUSE	Q4w655	mus musculus	483	193.5	6.2	893	2	Q96C25	HUMAN	Q96c25	homo sapien
411	201	6.4	430	2	Q5F120	HOMO SAPIEN	Q5f120	homo sapien	484	193.5	6.2	910	2	Q9HB75	HUMAN	Q9hb75	homo sapien
412	201	6.4	581	2	Q9BTR7	HUMAN	Q9btr7	homo sapien	485	193.5	6.2	977	1	SLIK3	HUMAN	SLIK3	homo sapien
413	201	6.4	602	2	Q9H9A6	HUMAN	Q9h9a6	homo sapien	486	193	6.2	252	2	Q4G1I2	EPTST	Q4g1i2	epitretus
414	201	6.4	712	2	Q5BL20	BRARE	Q5bl20	brachydanio	487	193	6.2	497	2	Q4SZU8	TETNG	Q4szu8	tetraodon n
415	200.5	6.4	845	1	SLIK2	HUMAN	Q9h156	homo sapien	488	193	6.2	540	2	Q9NK84	DROME	Q9nk84	drosophila
416	200	6.4	460	2	Q4RK03	TETNG	Q4rk03	tetraodon n	489	193	6.2	550	2	Q9VJN8	DROME	Q9vjn8	drosophila
417	200	6.4	616	2	Q5A9A5	CABEL	Q5a9a5	caenorhabdi	490	192.5	6.1	187	2	Q6E4D5	PETMA	Q6e4d5	petromyzon
418	200	6.4	653	2	Q02329	CABEL	Q02329	caenorhabdi	491	192.5	6.1	214	2	Q6E4G0	PETMA	Q6e4g0	petromyzon
419	199.5	6.4	227	2	Q4SP28	TETNG	Q4sp28	tetraodon n	492	192.5	6.1	259	2	Q4G1H7	EPTST	Q4g1h7	epitretus
420	199.5	6.4	261	2	Q4G1L4	EPTBU	Q4g1l4	epitretus	493	192.5	6.1	270	2	Q6E4K0	PETMA	Q6e4k0	petromyzon
421	199.5	6.4	622	2	Q66HV5	BRARE	Q66hv5	brachydanio	494	192.5	6.1	428	2	Q6GU68	MOUSE	Q6gu68	mus musculus
422	199	6.3	846	1	SLIK2	MOUSE	Q810c0	mus musculus	495	192.5	6.1	542	2	Q50D27	MOUSE	Q50d27	mus musculus
423	199	6.3	862	2	Q4SST3	TETNG	Q4sst3	tetraodon n	496	192.5	6.1	575	2	Q23580	CABEL	Q23580	caenorhabdi
424	199	6.3	1328	2	Q21043	CABEL	Q21043	caenorhabdi	497	192.5	6.1	1093	3	Q6HA06	CRAIG	Q6ha06	crassostrea
425	198.5	6.3	259	2	Q4G1J4	EPTST	Q4g1j4	epitretus	498	192	6.1	265	2	Q6E4K2	PETMA	Q6e4k2	petromyzon
426	198.5	6.3	320	2	Q6YN44	HUMAN	Q6yn44	homo sapien	499	192	6.1	273	2	Q6E4C5	PETMA	Q6e4c5	petromyzon
427	198.5	6.3	617	1	L8C21	RAT	Q9jmh2	rattus norv	500	192	6.1	548	1	LG13	MOUSE	Q8k406	mus musculus
428	198.5	6.3	741	2	Q4SWG9	TETNG	Q4swg9	tetraodon n	501	192	6.1	627	2	Q6UNI4	LEICH	Q6uni4	leishmania
429	198.5	6.3	873	2	Q7XR24	ORYZA	Q7xr24	oryza sativ	502	191.5	6.1	187	2	Q6E4I7	PETMA	Q6e4i7	petromyzon
430	198.5	6.3	1331	1	LG124	HUMAN	Q9p6p1	homo sapien	503	191.5	6.1	204	2	Q6E4J8	PETMA	Q6e4j8	petromyzon
431	198	6.3	363	2	Q7SYE5	BRARE	Q7syey5	brachydanio	504	191.5	6.1	915	2	Q9ERV7	MOUSE	Q9erv7	mus musculus
432	198	6.3	602	2	Q8FEB9	PONPY	Q5fey9	pongo pygma	505	191.5	6.1	980	1	SLIK3	MOUSE	Q610b9	mus musculus
433	197.5	6.3	300	2	Q6E4K3	PETMA	Q6e4k3	petromyzon	506	191.5	6.1	980	2	Q6NZM5	MOUSE	Q6nmz5	mus musculus
434	197.5	6.3	300	2	Q6E4K0	PETMA	Q6e4k8	petromyzon	507	191	6.1	271	2	Q4KP00	LAMAP	Q4kp00	lampetra ap
435	197.5	6.3	441	2	Q4VBZ3	HUMAN	Q4vbz3	homo sapien	508	191	6.1	440	2	Q5RC08	FONPY	Q5rc08	pongo pygma
436	197.5	6.3	537	2	Q3VEA9	DROME	Q9ve49	drosophila	509	191	6.1	610	2	Q4TIM0	TETNG	Q4tim0	tetraodon n
437	197.5	6.3	548	1	LG13	HUMAN	Q8n145	homo sapien	510	190.5	6.1	251	2	Q4G1I7	EPTST	Q4g1i7	epitretus
438	197.5	6.3	548	2	Q4R4H3	MACFA	Q4r4h3	macaca fasc	511	190.5	6.1	894	2	Q5H721	FUGRU	Q5h721	fugu rubrip
439	197.5	6.3	818	2	Q4SIX2	TETNG	Q4s1x2	tetraodon n	512	190.5	6.1	1238	2	Q6NR19	DROME	Q6nr19	drosophila
440	197.5	6.3	835	2	Q4SFB0	TETNG	Q4sfb0	tetraodon n	513	190.5	6.1	1535	2	Q9VPF0	DROME	Q9vpf0	drosophila
441	197.5	6.3	1321	1	Q4SFB0	TETNG	Q81wk6	homo sapien	514	190	6.1	191	2	Q6E4H3	PETMA	Q6e4h3	petromyzon
442	197	6.3	345	2	Q9HBL6	HUMAN	Q9hbl6	homo sapien	515	190	6.1	639	2	Q4RE68	TETNG	Q4re68	tetraodon n
443	197	6.3	694	2	Q6YXX5	ORYZA	Q6yxx5	oryza sativ	516	190	6.1	654	2	Q628N6	CAEBR	Q628n6	caenorhabdi
444	197	6.3	1093	2	Q4XWD3	HUMAN	Q5xwd3	homo sapien	517	190	6.1	733	1	CT075	MOUSE	P59383	mus musculus
445	196.5	6.3	259	2	Q4G1J3	EPTST	Q4g1j3	epitretus	518	190	6.1	1119	1	LRIG3	HUMAN	Q6uxm1	homo sapien
446	196.5	6.3	261	2	Q4G1J1	EPTST	Q4g1j1	epitretus	519	190	6.1	1346	2	Q9V477	DROME	Q9v477	drosophila
447	196	6.3	263	2	Q6E4D0	PETMA	Q6e4d0	petromyzon	520	189.5	6.1	2800	2	Q6XHB1	DICDI	Q6xhb1	dictyosteli
448	196	6.3	3638	2	Q15142	HUMAN	Q15142	homo sapien	521	189.5	6.0	252	2	Q4G1J7	EPTST	Q4g1j7	epitretus
449	195.5	6.2	370	2	Q58DI7	BOVIN	Q58di7	bos taurus	522	189.5	6.0	370	2	Q4RSX9	TETNG	Q4rsx9	tetraodon n
450	195.5	6.2	378	1	PRELP	MOUSE	Q91k53	mus musculus	523	189	6.0	369	1	PGS1	MOUSE	P28653	mus musculus
451	195.5	6.2	378	2	Q543S0	MOUSE	Q543s0	mus musculus	524	189	6.0	369	1	PGS1	RAT	P47853	rattus norv
452	195.5	6.2	917	2	Q6PML	DROME	Q86pml	drosophila	525	189	6.0	627	2	Q4TSR5	TETNG	Q4tsr5	tetraodon n
453	195.5	6.2	931	2	Q9VW16	DROME	Q9vw16	drosophila	526	189	6.0	760	2	Q4QGI8	LEIMA	Q4qgi8	leishmania
454	195	6.2	440	2	Q4R5H2	MACFA	Q4r5h2	macaca fasc	527	189	6.0	839	2	Q9SN46	ARATH	Q9sn46	arabidopsis
455	195	6.2	614	2	Q6NUK3	HUMAN	Q6nuk3	homo sapien	528	189	6.0	1392	2	Q9VAD1	DROME	Q9vad1	drosophila
456	195	6.2	620	2	Q6DXM3	HUMAN	Q6uxm3	homo sapien	529	189	6.0	4311	2	Q7YQK5	CANFA	Q7yqk5	canis fami
457	195	6.2	837	2	SLIK4	HUMAN	Q81w52	homo sapien	530	188.5	6.0	369	2	Q6GMI5	BRARE	Q6gmi5	brachydanio
458	195	6.2	837	2	Q5UXG3	HUMAN	Q51xg3	homo sapien	531	188.5	6.0	370	2	Q504E0	BRARE	Q504e0	brachydanio
459	194.5	6.2	369	2	Q65Z91	CHICK	Q65z91	gallus gall	532	188.5	6.0	410	2	Q3DDZ7	PETMA	Q3ddz7	petromyzon
460	194.5	6.2	693	2	Q7Z3D0	HUMAN	Q7z3d0	homo sapien	533	188.5	6.0	433	2	Q5SYH5	MOUSE	Q5syh5	mus musculus
461	194.5	6.2	699	1	ECW2	HUMAN	Q94769	homo sapien	534	188.5	6.0	440	1	OMGP	MOUSE	Q63912	mus musculus
462	194.5	6.2	699	2	Q5T9F2	HUMAN	Q5t9f2	homo sapien	535	188.5	6.0	538	2	Q5Z8W0	ORYZA	Q5z8w0	oryza sativ
463	194.5	6.2	737	2	Q965M3	CABEL	Q965m3	caenorhabdi	536	188.5	6.0	655	2	Q4SBU9	TETNG	Q4sbu9	tetraodon n
464	194.5	6.2	881	2	Q965M2	CABEL	Q965m2	caenorhabdi	537	188	6.0	368	2	Q53HU6	HUMAN	Q53hu6	homo sapien
465	194.5	6.2	1630	1	LAP4	HUMAN	Q14160	homo sapien	538	188	6.0	369	1	PGS1	CANFA	Q02678	canis fami
466	194	6.2	258	2	Q4G1J0	EPTST	Q4g1j0	epitretus	539	188	6.0	369	2	Q7TMM3	MOUSE	Q7tmw3	mus musculus
467	194	6.2	258	2	Q4G1I0	EPTST	Q4g1i0	epitretus	540	188	6.0	522	1	LRTM1	MOUSE	Q8k377	mus musculus
468	194	6.2	263	2	Q6E4C0	PETMA	Q6e4c0	petromyzon	541	188	6.0	626	2	Q4SE92	TETNG	Q4se92	tetraodon n
469	194	6.2	611	2	Q4RHK3	TETNG	Q4rhk3	tetraodon n	542	188	6.0	818	2	Q5ZIH8	CHICK	Q5zih8	gallus gall

543	187.5	6.0	259	2	Q4G110_EPTBU	Q4g110 eptatretus
544	187.5	6.0	310	2	Q3DD28_PETMA	Q3dd28 petromyzon
545	187.5	6.0	350	2	Q5M789_XENTR	Q5m789 xenopus tro
546	187.5	6.0	352	2	Q4W6V7_CHICK	Q4w6v7 gallus gall
547	187.5	6.0	363	2	Q3H5G9_HUMAN	Q3h5g9 homo sapien
548	187.5	6.0	425	2	Q3VGH2_DROME	Q3vgh2 drosophila
549	187.5	6.0	601	2	Q7SXW3_BRARE	Q7sxw3 brachydanio
550	187.5	6.0	861	2	Q4ZJ82_CHICK	Q4zj82 gallus gall
551	187	6.0	260	2	Q4G1K7_EPTST	Q4g1k7 eptatretus
552	187	6.0	262	2	Q4G1K0_EPTST	Q4g1k0 eptatretus
553	187	6.0	592	2	Q61PG4_CAEBR	Q61pg4 caenorhabdi
554	187	6.0	615	2	Q3VZB4_DROME	Q3vzb4 drosophila
555	187	6.0	735	2	Q6E1I4_MOUSE	Q6e1i4 mus musculus
556	187	6.0	818	2	Q5WA51_CHICK	Q5wa51 gallus gall
557	187	6.0	1741	2	Q5LJU2_DROME	Q5lju2 drosophila
558	186.5	5.9	368	1	PGS1_XENLA	Q9ib75 xenopus lae
559	186.5	5.9	521	2	Q72U34_LEPIC	Q72u34 leptospira
560	186.5	5.9	639	2	Q5VZ17_HUMAN	Q5vzi7 homo sapien
561	186.5	5.9	799	2	Q5VZ18_HUMAN	Q5vzi8 homo sapien
562	186.5	5.9	839	1	TLR4_PANPA	Q9tt20 pan paniscu
563	186.5	5.9	839	1	TLR4_PANPA	Q5vzi9 homo sapien
564	186.5	5.9	839	1	Q5VZ19_HUMAN	Q5vzi9 homo sapien
565	186	5.9	273	2	Q6E4B4_PETMA	Q6e4b4 petromyzon
566	186	5.9	368	2	Q5RAV4_PONPY	Q5ray4 pongo pygma
567	186	5.9	440	1	OMGP_HUMAN	P23515 homo sapien
568	186	5.9	440	2	Q53HB8_HUMAN	Q53hb8 homo sapien
569	186	5.9	552	2	Q9VT44_DROME	Q9vt44 drosophila
570	186	5.9	623	1	LRC21_HUMAN	Q9p2v4 homo sapien
571	186	5.9	1029	2	Q5I2M5_BOVIN	Q5i2m5 bos taurus
572	185.5	5.9	369	2	Q4T3M1_TETNG	Q4t3m1 tetraodon n
573	185.5	5.9	466	2	Q6M1W3_XENLA	Q6m1w3 xenopus lae
574	185.5	5.9	953	2	Q6M1F7_PARUW	Q6mf87 parachlamyd
575	185	5.9	259	2	Q4S4N7_TETNG	Q4s4n7 tetraodon n
576	185	5.9	389	2	Q6PB55_BRARE	Q6pbp5 brachydanio
577	185	5.9	512	2	Q6PEZ8_HUMAN	Q6pez8 homo sapien
578	185	5.9	603	2	Q5ZLN0_CHICK	Q5zln0 gallus gall
579	184.5	5.9	257	2	Q4GL15_EPTBU	Q4gl15 eptatretus
580	184.5	5.9	270	2	Q4KP09_LAMAP	Q4kp09 lampetra ap
581	184.5	5.9	724	2	Q5XWB9_HORSE	Q5xwb9 equus caball
582	184.5	5.9	799	2	Q9V964_DROME	Q9v964 drosophila
583	184.5	5.9	839	2	Q6ZVU6_MOUSE	Q6zvuv6 mus musculus
584	184.5	5.9	841	2	Q5F4K7_PIG	Q5f4k7 sus scrofa
585	184.5	5.9	843	1	TLR4_HORSE	Q9my107 mus musculus
586	184.5	5.9	957	1	SLIK5_MOUSE	Q810b7 mus musculus
587	184.5	5.9	1007	2	Q65X83_ORYSA	Q65x83 oryza sativ
588	184.5	5.9	1046	2	Q5GQ97_CHICK	Q5gq97 gallus gall
589	184.5	5.9	1214	2	Q6JN06_ORYSA	Q6jng6 oryza sativ
590	184	5.9	187	2	Q6E4M5_PETMA	Q6e4m5 petromyzon
591	184	5.9	253	2	Q6E4K5_PETMA	Q6e4k5 petromyzon
592	184	5.9	263	2	Q6E4K7_PETMA	Q6e4k7 petromyzon
593	184	5.9	274	2	Q4G1M0_EPTBU	Q4g1m0 eptatretus
594	184	5.9	291	2	Q4RF21_TETNG	Q4rf21 tetraodon n
595	184	5.9	368	1	PGS1_HUMAN	P21810 homo sapien
596	184	5.9	368	2	Q53F14_HUMAN	Q53f14 homo sapien
597	184	5.9	473	2	Q7QF76_ANOGA	Q7qf76 anopheles g
598	184	5.9	543	2	Q4RG66_TETNG	Q4rg66 tetraodon n
599	184	5.9	552	2	Q6K6X6_ORYSA	Q6k6x6 oryza sativ
600	184	5.9	565	2	Q7PJ00_ANOGA	Q7pj00 anopheles g
601	184	5.9	837	1	SLIK4_MOUSE	Q810b8 mus musculus
602	183.5	5.9	187	2	Q6E4F6_PETMA	Q6e4f6 petromyzon
603	183.5	5.9	287	2	Q9W2B9_DROME	Q9w2b9 drosophila
604	183.5	5.9	292	2	Q6NTY6_BRARE	Q6nty6 brachydanio
605	183.5	5.9	601	2	Q6TLH1_BRARE	Q6tlh1 brachydanio
606	183.5	5.9	652	2	Q7Q696_ANOGA	Q7q696 anopheles g
607	183.5	5.9	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculus
608	183.5	5.9	795	1	TLR1_MOUSE	Q9epq1 mus musculus
609	183.5	5.9	824	1	Q5GGX1_PIG	Q5ggx1 sus scrofa
610	183.5	5.9	841	1	TLR4_PIG	Q68y56 sus scrofa
611	183.5	5.9	1059	2	Q5ZJD0_CHICK	Q5zjd0 gallus gall
612	183.5	5.9	1495	2	Q5VXC2_HUMAN	Q5vxc2 homo sapien
613	183.5	5.9	1537	1	LRR7_HUMAN	Q96nw7 homo sapien
614	183.5	5.9	1537	2	Q5VXC3_HUMAN	Q5vxc3 homo sapien
615	183	5.8	540	2	Q9VU53_DROME	Q9vu53 drosophila

Q6p3y9 mus musculus	568	5.8	183	616
Q14392 homo sapien	568	5.8	183	617
Q7zt81 oncorhynch	664	5.8	183	618
Q5zj34 gallus gall	664	5.8	183	619
Q6e4g1 petromyzon	187	5.8	182.5	620
Q6e4g7 petromyzon	187	5.8	182.5	621
Q4g1l8 eptatretus	257	5.8	182.5	622
Q9bxx1 homo sapien	379	5.8	182.5	623
Q5tbf3 homo sapien	380	5.8	182.5	624
Q6p528 homo sapien	384	5.8	182.5	625
Q8t3j2 drosophila	810	5.8	182.5	626
Q9vks4 drosophila	811	5.8	182.5	627
Q8ep98 pongo pygma	828	5.8	182.5	628
Q9v848 drosophila	837	5.8	182.5	629
Q8ep88 gorilla gor	880	5.8	182.5	630
P91643 drosophila	958	5.8	182.5	631
Q94991 homo sapien	958	5.8	182.5	632
Q5vt81 homo sapien	958	5.8	182.5	633
Q4qhl1 homo sapien	958	5.8	182.5	634
Q4r9x7 tetraodon n	205	5.8	182	635
Q4g1l8 eptatretus	252	5.8	182	636
Q6e4c4 petromyzon	271	5.8	182	637
Q4ru73 tetraodon n	297	5.8	182	638
Q46390 ovis aries	369	5.8	182	639
Q5bim3 bos taurus	369	5.8	182	640
Q803t1 brachydanio	373	5.8	182	641
Q5ri45 brachydanio	373	5.8	182	642
Q8f3f8 leptospira	428	5.8	182	643
Q96671 drosophila	532	5.8	182	644
Q7q550 anopheles g	678	5.8	182	645
Q8xv0 bos taurus	1022	5.8	182	646
Q866b2 bos taurus	1029	5.8	182	647
Q8bp10 mus musculus	180	5.8	181.5	648
Q4g1k2 eptatretus	251	5.8	181.5	649
Q4g1j8 eptatretus	259	5.8	181.5	650
P28675 gallus gall	337	5.8	181.5	651
Q7t3h6 brachydanio	599	5.8	181.5	652
Q61pg3 caenorhabdi	699	5.8	181.5	653
O13328 magnaporthe	2160	5.8	181.5	654
O13488 magnaporthe	2160	5.8	181.5	655
Q51j05 magnaporthe	2160	5.8	181	656
Q46403 equus caball	372	5.8	181	657
Q7qip3 anopheles g	569	5.8	181	658
Q8lq10 oryza sativ	1013	5.8	180	659
Q7qif68 anopheles g	1333	5.8	181	660
Q6gl06 xenopus lae	371	5.8	180.5	661
Q8bmw6 mus musculus	385	5.8	180.5	662
Q8l170 drosophila	441	5.8	180.5	663
Q5r7m3 pongo pygma	522	5.8	180.5	664
Q6pgx3 brachydanio	584	5.8	180.5	665
Q96py3 homo sapien	821	5.8	180.5	666
Q9vj00 drosophila	1443	5.8	180.5	667
Q5hz61 xenopus tro	1460	5.8	180.5	668
Q4gim2 eptatretus	250	5.7	180	669
P21809 bos taurus	369	5.7	180	670
Q5r6b1 pongo pygma	522	5.7	180	671
Q86p15 drosophila	817	5.7	180	672
Q9v84 drosophila	817	5.7	180	673
Q7ztg5 gallus gall	843	5.7	180	674
Q4s0c1 tetraodon n	869	5.7	179.5	675
Q6e4d6 petromyzon	187	5.7	179.5	676
Q61gx3 caenorhabdi	585	5.7	179.5	677
Q5r3f8 homo sapien	820	5.7	179.5	678
Q6p1c6 mus musculus	1117	5.7	179	679
Q9erv0 rattus norv	4283	5.7	179	680
Q6e4b8 petromyzon	273	5.7	179	681
Q5mbm9 mus musculus	314	5.7	179	682
Q9vt89 drosophila	534	5.7	179	683
Q9p244 homo sapien	700	5.7	179	684
Q9bjd4 strongyloce	742	5.7	179	685
Q9mb1 mus musculus	905	5.7	179	686
Q4lbc9 oncorhynch	969	5.7	179	687
Q512m4 ovis aries	1029	5.7	179	688
Q56715 brachydanio	176	5.7	178.5	689

689	178.5	5.7	190	2	Q6A4D8_PETMA	Q6e4d8	petromyzon	762	174.5	5.6	440	2	Q4J5V4_AZOVI	Q4j5v4	azotobacter
690	178.5	5.7	348	2	QSR143_BRARE	Q5i4i3	brachydanio	763	174.5	5.6	512	2	Q9C076_MOUSE	Q9c076	m mus muscu
691	178.5	5.7	356	1	PGS2_COTJA	Q9de68	coturnix co	764	174.5	5.6	567	2	Q4SL10_TETNG	Q4sl10	tetraodon n
692	178.5	5.7	443	1	Q67VV7_ORISA	Q67vv7	oryza sativ	765	174.5	5.6	602	2	Q9CRC8_MOUSE	Q9crc8	mus musculus
693	178.5	5.7	493	1	ANGOL1_HUMAN	Q86wk6	homo sapien	766	174.5	5.6	602	2	Q8BS83_MOUSE	Q8bs83	mus musculus
694	178.5	5.7	587	2	Q4QGJ9_LEIMA	Q4qgj9	leishmania	767	174.5	5.6	602	2	Q78WQ9_MOUSE	Q78wq9	mus musculus
695	178.5	5.7	1024	1	POPC_RALSO	Q9rb82	ralstonia s	768	174.5	5.6	605	2	Q6GRJ5_XENLA	Q6grp5	xenopus lae
696	178.5	5.7	1063	2	Q5Z666_ORISA	Q5z666	oryza sativ	769	174.5	5.6	795	1	TLR6_MOUSE	Q9epw9	mus musculus
697	178.5	5.7	1104	2	Q7XUH4_ORISA	Q7xuh4	oryza sativ	770	174.5	5.6	1020	2	Q5ZED4_ORISA	Q5zed4	oryza sativ
698	178.5	5.7	1310	1	G1215_MOUSE	Q7ctt36	mus musculus	771	174.5	5.6	1060	2	Q6ZGM3_ORISA	Q6zgm3	oryza sativ
699	178	5.7	187	2	Q6E4H4_PETMA	Q6e4h4	petromyzon	772	174	5.6	490	2	Q4RYL5_TETNG	Q4ryl5	tetraodon n
700	178	5.7	364	2	Q66J59_XENLA	Q66j59	xenopus lae	773	174	5.6	535	2	Q8RX50_BRANI	Q8rx50	brassica ni
701	178	5.7	391	2	Q4RQ11_TETNG	Q4rq11	tetraodon n	774	174	5.6	544	2	Q7Q2W5_ANOGA	Q7q2w5	anopheles g
702	178	5.7	488	2	Q4RXQ5_TETNG	Q4rxq5	tetraodon n	775	174	5.6	651	2	Q4JQO2_XENLA	Q4jqo2	xenopus lae
703	178	5.7	522	1	LRTM1_HUMAN	Q8ue6	homo sapien	776	174	5.6	859	1	TLR5_MOUSE	Q9jlf7	mus musculus
704	178	5.7	894	2	Q9BJD6_STRPU	Q9bjd6	strongyloce	777	174	5.6	951	1	LGR4_RAT	Q9z2h4	rattus norv
705	178	5.7	1049	1	TLR7_HUMAN	Q9nyk1	homo sapien	778	173.5	5.5	261	2	Q5M8T1_HUMAN	Q5m8t1	homo sapien
706	178	5.7	1052	2	Q9Y4C4_HUMAN	Q9y4c4	homo sapien	779	173.5	5.5	337	2	Q4RJX0_TETNG	Q4rjx0	tetraodon n
707	178	5.7	1257	2	Q7PNF8_ANOGA	Q7pnf8	anopheles g	780	173.5	5.5	353	2	Q640B1_XENTR	Q640b1	xenopus tro
708	177.5	5.7	275	2	Q4GLK5_EPTST	Q4glk5	eptatretus	781	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8	xenopus lae
709	177.5	5.7	796	2	Q59H19_PIG	Q59h19	sus scrofa	782	173.5	5.5	421	1	OMD_HUMAN	Q99n83	homo sapien
710	177.5	5.7	796	2	Q4LDR7_PIG	Q4ldr7	sus scrofa	783	173.5	5.5	421	2	Q5TBF4_HUMAN	Q5tbf4	homo sapien
711	177.5	5.7	809	2	Q4RMQ1_TETNG	Q4rmq1	tetraodon n	784	173.5	5.5	440	2	Q7TQ25_RAT	Q7tq25	rattus norv
712	177.5	5.7	1026	2	Q5SMW2_ORISA	Q5smw2	oryza sativ	785	173.5	5.5	537	1	LGI4_MOUSE	Q8klsl	mus musculus
713	177.5	5.7	1050	1	TLR7_MOUSE	P59681	mus musculus	786	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21	bos taurus
714	177.5	5.7	1050	2	Q548J0_MOUSE	Q548j0	mus musculus	787	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7tpc5	mus musculus
715	177.5	5.7	1360	2	Q7KTA0_DROME	Q7kta0	drosophila	788	173.5	5.5	826	1	TLR4_PAPAN	Q7scp2	papio anubi
716	177.5	5.7	1530	2	Q68D07_HUMAN	Q68d07	homo sapien	789	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720	fugu rubrip
717	177.5	5.7	2300	1	CVAA_NEUCR	Q01631	neurospora	790	173	5.5	252	2	Q4GL14_EPTST	Q4gl14	eptatretus
718	177.5	5.7	2493	1	CVAA_USTWA	P49606	ustilago ma	791	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2	petromyzon
719	177.5	5.7	2493	2	Q4P3T1_USTMA	Q4p3t1	ustilago ma	792	173	5.5	360	1	PGS2_HORSE	Q46542	equus cabal
720	177	5.6	187	2	Q4E4H5_PETMA	Q6e4h5	petromyzon n	793	173	5.5	470	2	Q9V354_DROME	Q9v354	drosophila
721	177	5.6	334	2	Q4SBU8_TETNG	Q4sbu8	tetraodon n	794	173	5.5	539	2	Q503F6_BRARE	Q503f6	brachydanio
722	177	5.6	343	1	LUM_COTJA	Q9de67	coturnix co	795	173	5.5	664	2	Q5UT54_SALSA	Q5ut54	salmo salar
723	177	5.6	347	2	Q58A48_BRARE	Q58a48	brachydanio	796	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40	mus musculus
724	177	5.6	662	2	Q5RF01_PONPY	Q5rf01	pongo pygma	797	173	5.5	925	1	GLHR_ANTLR	P35409	anthopleura
725	177	5.6	666	2	Q7Q2W6_ANOGA	Q7q2w6	anopheles g	798	173	5.5	1459	2	Q7Q0C5_ANOGA	Q7q0c5	anopheles g
726	177	5.6	670	2	Q5FW85_MOUSE	Q5fw85	mus musculus	799	173	5.5	1459	2	Q8WRE4_ANOGA	Q8wre4	anopheles g
727	177	5.6	1370	2	Q58N44_APIME	Q58n44	apis mellif	800	172.5	5.5	163	2	Q6E4E2_PETMA	Q6e4e2	petromyzon
728	176.5	5.6	187	2	Q4SBD4_PETMA	Q6e4m0	petromyzon	801	172.5	5.5	353	1	KERA_CHICK	Q42235	gallus gall
729	176.5	5.6	520	2	Q5VR46_ORISA	Q5vr46	oryza sativ	802	172.5	5.5	353	1	KERA_COTJA	Q9de66	coturnix co
730	176.5	5.6	522	1	ANGO2_HUMAN	Q86sj2	homo sapien	803	172.5	5.5	359	1	PGS2_HUMAN	P07585	homo sapien
731	176.5	5.6	522	2	Q4VBP6_HUMAN	Q4vbp6	homo sapien	804	172.5	5.5	359	1	PGS2_PANTR	Q5rlv9	pan troglod
732	176.5	5.6	628	2	Q7PVC6_ANOGA	Q7pvc6	anopheles g	805	172.5	5.5	359	2	Q6FH10_HUMAN	Q6fhl0	homo sapien
733	176.5	5.6	856	2	Q59H17_PIG	Q59h17	sus scrofa	806	172.5	5.5	378	2	Q5R294_DROSI	Q5r294	drosophila
734	176.5	5.6	901	2	Q4SBD4_TETNG	Q4sbd4	tetraodon n	807	172.5	5.5	739	2	Q60NV9_CAEBR	Q60nv9	caenorhabdi
735	176.5	5.6	1495	1	LRRCT7_RAT	P70587	rattus norv	808	172.5	5.5	823	2	Q8CCW8_MOUSE	Q8ccw8	mus musculus
736	176.5	5.6	1756	2	Q6AWK6_DROME	Q6awk6	drosophila	809	172.5	5.5	823	2	Q68FM6_MOUSE	Q68fm6	mus musculus
737	176	5.6	249	2	Q4SUM4_TETNG	Q4sum4	tetraodon n	810	172.5	5.5	1711	2	Q59DT7_DROME	Q59dt7	drosophila
738	176	5.6	503	2	Q8LJ87_ORISA	Q8lj87	oryza sativ	811	172.5	5.5	1850	2	Q59DT8_DROME	Q59dt8	drosophila
739	176	5.6	623	2	Q5S821_DROME	Q5s821	drosophila	812	172.5	5.5	1851	1	LAP4_DROME	Q8kry7	drosophila
740	176	5.6	862	2	Q5GR02_CHICK	Q5gr02	gallus gall	813	172.5	5.5	4256	2	Q8MGF3_CANFA	Q8mjf3	canis fami
741	176	5.6	904	2	Q5TJ59_BOVIN	Q5tj59	bos taurus	814	172	5.5	339	2	Q4SU68_TETNG	Q4su68	tetraodon n
742	176	5.6	905	2	Q5TJ58_BOVIN	Q5tj58	bos taurus	815	172	5.5	347	2	Q7ZUT1_BRARE	Q7zut1	brachydanio
743	176	5.6	906	2	Q4SR20_TETNG	Q4sr20	tetraodon n	816	172	5.5	411	2	Q4S9P3_TETNG	Q4s9p3	tetraodon n
744	176	5.6	1032	2	Q5I2M8_CANFA	Q5i2m8	canis fami	817	172	5.5	577	2	Q8N3K5_HUMAN	Q8n3k5	homo sapien
745	176	5.6	1257	2	Q9VK28_DROME	Q9vk28	drosophila	818	172	5.5	1134	2	Q65510_ARATH	Q65510	arabidopsis
746	176	5.6	1412	1	LAP2_HUMAN	Q9grt1	homo sapien	819	172	5.5	1693	2	Q4INH4_GIBZE	Q4inh4	gibberella
747	175.5	5.6	272	2	Q4KP14_PETMR	Q4kpl14	ichthyomyzo	820	171.5	5.5	378	2	Q9V900_DROME	Q9v900	drosophila
748	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4	tetraodon n	821	171.5	5.5	605	2	Q5M8G4_XENTR	Q5m8g4	xenopus tro
749	175.5	5.6	440	2	Q7TNM3_RAT	Q7tnm3	rattus norv	822	171.5	5.5	683	1	LRCM4_HUMAN	Q75427	homo sapien
750	175.5	5.6	492	1	ANGOL1_MOUSE	Q80zd8	mus musculus	823	171.5	5.5	858	1	TLR5_HUMAN	Q60602	homo sapien
751	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718	fugu rubrip	824	171.5	5.5	858	2	Q5U308_RAT	Q5u308	rattus norv
752	175.5	5.6	1490	1	LRRCT7_MOUSE	Q80te7	mus musculus	825	171.5	5.5	859	1	LRRCS_MOUSE	Q8bgr2	mus musculus
753	175.5	5.6	1731	2	Q4S0D3_TETNG	Q4s0d3	tetraodon n	826	171.5	5.5	1589	2	Q9UUQ9_METAN	Q9uuq9	metathizium
754	175	5.6	252	2	Q4GLJ2_EPTST	Q4glj2	eptatretus	827	171	5.5	360	1	PGS2_PIG	Q9xsd9	sus scrofa
755	175	5.6	343	1	LUM_CHICK	P51890	gallus gall	828	171	5.5	360	2	Q6DVI1_GEGJA	Q6dvi1	gecko japon
756	175	5.6	429	2	Q8BJ09_MOUSE	Q8bj09	mus musculus	829	171	5.5	552	2	Q86V06_HUMAN	Q86v06	homo sapien
757	175	5.6	510	2	Q9BGY6_MACFA	Q9bgy6	macaca fasc	830	171	5.5	643	2	Q502J4_BRARE	Q502j4	brachydanio
758	175	5.6	941	2	Q5H722_FUGRU	Q5h722	fugu rubrip	831	171	5.5	833	1	TLR4_FELCA	P38727	felis silve
759	175	5.6	973	2	Q6KCC7_ONCMY	Q6kcc7	oncorhynch	832	171	5.5	1317	2	Q5TUS9_ANOGA	Q5tus9	anopheles g
760	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1	anopheles g	833	170.5	5.4	246	2	Q6E4J1_PETMA	Q6e4j1	petromyzon
761	174.5	5.6	190	2	Q6E4E5_PETMA	Q6e4e5	petromyzon	834	170.5	5.4	359	2	Q4R5D2_MACFA	Q4r5d2	macaca fasc

835	170.5	5.4	373	1	ASPN_MOUSE	Q99mq4 mus musculus	908	167	5.3	1112	2	Q4G2W2_LYCPM	Q4g2w2 lycopersico
836	170.5	5.4	741	2	Q8KTF7_LISMO	Q8ktf7 listeria mo	909	167	5.3	1263	2	Q4SID1_TESTNG	Q4sid1 tetraodon n
837	170.5	5.4	1031	2	Q5I2M7_FELCA	Q5i2m7 felis silve	910	167	5.3	1845	2	Q5QNQ9_MOUSE	Q5qnq9 mus musculus
838	170.5	5.4	1031	2	Q8HZ52_FELCA	Q8hz52 felis silve	911	166.5	5.3	163	2	Q6E4D4_PETMA	Q6e4d4 petromyzon
839	170.5	5.4	2145	1	CYAA_PODAN	Q01513 podospora a	912	166.5	5.3	483	2	Q5NE36_LISMO	Q5ne36 listeria mo
840	170	5.4	187	2	Q6E4D9_PETMA	Q6e4d9 petromyzon	913	166.5	5.3	549	2	Q9SVW8_ARATH	Q9svw8 arabidopsis
841	170	5.4	364	1	LRC19_MOUSE	Q8bzt5 mus musculus	914	166.5	5.3	582	2	Q9SR423_PONPY	Q9sr423 pongo pygma
842	170	5.4	572	2	Q4QGJ6_LEIMA	Q4qgj6 leishmania	915	166.5	5.3	739	2	Q84CF6_LISMO	Q84cf6 listeria mo
843	170	5.4	883	2	Q4VAM0_HUMAN	Q4vam0 homo sapien	916	166.5	5.3	741	2	Q8KTF0_LISMO	Q8ktf0 listeria mo
844	170	5.4	907	1	LGR5_HUMAN	Q175473 homo sapien	917	166.5	5.3	741	2	Q8KTF9_LISMO	Q8ktf9 listeria mo
845	170	5.4	907	2	Q4VAM2_HUMAN	Q4vam2 homo sapien	918	166.5	5.3	743	2	Q95RV9_DROME	Q95rv9 drosophila
846	170	5.4	1024	2	Q84I86_RALSO	Q84ie6 halstonia s	919	166.5	5.3	743	2	Q8KTF2_LISMO	Q8ktf2 listeria mo
847	170	5.4	1032	2	Q9SER8_HUMAN	Q9ser8 homo sapien	920	166.5	5.3	744	2	Q8KHNI_LISMO	Q8khn1 listeria mo
848	170	5.4	1471	2	Q7KW92_DROME	Q7kw92 drosophila	921	166.5	5.3	744	2	Q8KI88_LISMO	Q8ki88 listeria mo
849	169.5	5.4	352	1	KERA_BOVIN	Q62702 bos taurus	922	166.5	5.3	744	2	Q8KTF1_LISMO	Q8ktf1 listeria mo
850	169.5	5.4	366	2	Q8BX06_MOUSE	Q8bx06 m mus muscu	923	166.5	5.3	744	2	Q8KTF5_LISMO	Q8ktf5 listeria mo
851	169.5	5.4	493	1	ANGOL_RAT	Q80x06 m mus muscu	924	166.5	5.3	744	2	Q8KTF8_LISMO	Q8ktf8 listeria mo
852	169.5	5.4	651	2	Q4T8T9_TETNG	Q80zdt rattus norv	925	166.5	5.3	746	2	Q8KTF3_LISMO	Q8ktf3 listeria mo
853	169.5	5.4	760	2	Q9T0K5_ARATH	Q8t8t9 tetraodon n	926	166.5	5.3	792	2	Q5NE37_LISMO	Q5ne37 listeria mo
854	169.5	5.4	876	2	Q67W85_ORYSA	Q9t0k5 arabidopsis	927	166.5	5.3	800	1	INLA_LISMF	Q723k6 listeria mo
855	169.5	5.4	991	2	Q6R5N8_MOUSE	Q6twe5 oryza sativ	928	166.5	5.3	800	1	INLA_LISMF	Q723k6 listeria mo
856	169.5	5.4	1271	1	FLII_MOUSE	Q6r5n8 mus musculus	929	166.5	5.3	800	1	INLA_LISMF	Q723k6 listeria mo
857	169	5.4	217	2	Q66WJ6_FELCA	Q9ij28 mus musculus	930	166.5	5.3	1012	2	Q95VT6_ASTPE	Q95vt6 asterina pe
858	169	5.4	273	2	Q8XPX6_ICTPU	Q66wj6 felis silve	931	166.5	5.3	1115	2	Q652D9_ORYSA	Q652d9 oryza sativ
859	169	5.4	279	2	Q58HK2_TRASC	Q8xp6 ictalurus p	932	166.5	5.3	1215	2	Q60PY2_CAEBR	Q60py2 caenorhabdi
860	169	5.4	354	1	PGS2_MOUSE	Q58hk2 trachemys s	933	166.5	5.3	1270	2	Q7QHP7_ANOAG	Q7qhp7 anopheles g
861	169	5.4	360	2	Q67OY6_PAROL	P28654 mus musculus	934	166.5	5.3	1280	2	Q95YI7_ASTPE	Q95yi7 asterina pe
862	169	5.4	757	2	Q69MS7_ORYSA	Q6j0y6 paralichthy	935	166	5.3	3204	2	Q6X248_9ALPH	Q6x248 bovine herp
863	169	5.4	839	2	Q9MS7_DEIRA	Q69ms7 oryza sativ	936	166	5.3	163	2	Q6E4F8_PETMA	Q6e4f8 petromyzon
864	169	5.4	1175	2	Q4RER3_TETNG	Q9rx57 deinococcus	937	166	5.3	245	2	Q4KP01_LAMAP	Q4kp01 lampetra ap
865	169	5.4	1288	2	Q624K5_CAEBR	Q4rer3 tetraodon n	938	166	5.3	426	2	Q72TC3_LEPIC	Q72tc3 leptospira
866	169	5.4	1658	2	Q4PLB9_FUSPR	Q624k5 caenorhabdi	939	166	5.3	806	2	Q4S8E3_TETNG	Q4sse3 tetraodon n
867	168.5	5.4	246	2	Q4KP10_LAMAP	Q4ple9 fusarium pr	940	166	5.3	835	1	TLR4_RAT	Q6p690 rattus norv
868	168.5	5.4	255	2	Q66WJ3_FELCA	Q4kp10 lampetra ap	941	166	5.3	1030	2	Q5I2M3_PIG	Q5i2m3 rattus norv
869	168.5	5.4	333	2	Q4SYZ8_TETNG	Q66wj3 felis silve	942	166	5.3	1030	2	Q865R8_FIG	Q865r8 sus scrofa
870	168.5	5.4	343	2	Q50I83_BRARE	Q4sy28 tetraodon n	943	166	5.3	1110	2	Q7G768_ORYSA	Q7g768 oryza sativ
871	168.5	5.4	353	2	Q7SY58_XENLA	Q50i83 brachydanio	944	166	5.3	1110	2	Q94LN2_ORYSA	Q94ln2 oryza sativ
872	168.5	5.4	363	2	Q8C8A7_MOUSE	Q7sy58 xenopus lae	945	166	5.3	1221	2	Q9N5Z3_CAEBL	Q9n5z3 caenorhabdi
873	168.5	5.4	378	2	Q5R264_DROSE	Q8c8a7 mus musculus	946	166	5.3	2139	2	Q4PDW0_USTWA	Q4pdw0 ustilago ma
874	168.5	5.4	619	2	Q6K8K0_ORYSA	Q5r264 drosophila	947	165.5	5.3	327	2	Q5RHE5_BRARE	Q5rhes brachydanio
875	168.5	5.4	685	2	Q6T545_LISMO	Q6k8k0 oryza sativ	948	165.5	5.3	360	1	PGS2_BOVIN	P21793 bos taurus
876	168.5	5.4	694	2	Q6IP91_CAEBR	Q6t545 listeria mo	949	165.5	5.3	360	1	PGS2_CANFA	Q93933 canis fami
877	168.5	5.4	728	2	Q6T546_LISMO	Q6ip91 caenorhabdi	950	165.5	5.3	526	2	Q7XJ53_ARATH	Q7xj53 arabidopsis
878	168.5	5.4	744	2	Q8KTF6_LISMO	Q6t546 listeria mo	951	165.5	5.3	641	2	Q5H716_FUGRU	Q5h716 fugu rubrip
879	168.5	5.4	907	1	LGR5_MOUSE	Q8ktf6 listeria mo	952	165.5	5.3	1101	2	Q5H9H5_HUMAN	Q5h9h5 homo sapien
880	168.5	5.4	1036	2	Q9FN37_ARATH	Q9z1p4 mus musculus	953	165.5	5.3	1256	1	FLII_DROME	Q24020 drosophila
881	168.5	5.4	1360	2	Q9ND11_DROME	Q9fn37 arabidopsis	954	165.5	5.3	1269	1	FLII_HUMAN	Q13045 homo sapien
882	168.5	5.4	1724	2	Q4H4B6_BRARE	Q9nd11 drosophila	955	165.5	5.3	1269	2	Q5R4G9_PONPY	Q5r4g9 pongo pygma
883	168	5.4	351	2	Q65YW8_XENLA	Q4h4b6 brachydanio	956	165	5.3	283	2	Q4RX02_TETNG	Q4rx02 tetraodon n
884	168	5.4	402	2	Q72U35_LEPIC	Q65yw8 xenopus lae	957	165	5.3	436	2	Q5R6F8_PONPY	Q5r6f8 pongo pygma
885	168	5.4	753	2	Q9NR56_HUMAN	Q72u35 leptospira	958	165	5.3	902	2	Q7RVP2_NEUCR	Q7rvp2 neurospora
886	168	5.4	773	2	Q5NE35_LISMO	Q9nre6 homo sapien	959	165	5.3	994	2	Q9C637_ARATH	Q9c637 arabidopsis
887	168	5.4	951	1	LGR4_HUMAN	Q5ne35 listeria mo	960	165	5.3	1135	2	Q7X512_ORYSA	Q7x512 oryza sativ
888	168	5.4	977	2	Q8GVW0_ORYSA	Q9bxb1 homo sapien	961	165	5.3	1154	2	Q7QHH4_ANOAG	Q7qh4 anopheles g
889	167.5	5.3	147	2	Q9TTO0_PIG	Q8gvw0 oryza sativ	962	164.5	5.2	235	2	Q4GLH9_EPTST	Q4gli9 eptaretus
890	167.5	5.3	351	1	KERA_MOUSE	Q9tto0 sus scrofa	963	164.5	5.2	468	2	Q4LVE2_9BURK	Q4lve2 burkholderi
891	167.5	5.3	360	1	PGS2_SHEEP	Q35367 mus musculus	964	164.5	5.2	582	1	SHOC2_HUMAN	Q5uq13 homo sapien
892	167.5	5.3	378	2	Q72U36_LEPIC	Q35367 mus musculus	965	164.5	5.2	582	2	Q5VZS9_HUMAN	Q5vz59 pongo pygma
893	167.5	5.3	396	2	Q8C3D9_MOUSE	Q72u36 leptospira	966	164.5	5.2	582	2	Q5RAV5_PONPY	Q5rav5 pongo pygma
894	167.5	5.3	422	1	OND_BOVIN	Q8c3d9 mus musculus	967	164.5	5.2	734	2	Q5R7N1_PONPY	Q5r7n1 pongo pygma
895	167.5	5.3	694	2	Q4RY12_TETNG	Q77742 bos taurus	968	164.5	5.2	805	2	Q658W7_HUMAN	Q658w7 homo sapien
896	167.5	5.3	917	2	Q75GM9_ORYSA	Q4ry12 tetraodon n	969	164.5	5.2	819	2	Q659A9_HUMAN	Q659a9 homo sapien
897	167.5	5.3	1174	2	Q7X837_ORYSA	Q75gm9 oryza sativ	970	164.5	5.2	858	1	LRRCS_HUMAN	Q711w4 homo sapien
898	167	5.3	537	2	Q6P2A4_RAT	Q7x837 oryza sativ	971	164	5.2	257	1	LRRCS_MOUSE	P59034 mus musculus
899	167	5.3	582	2	Q8AY15_RAT	Q6p2a4 rattus norv	972	164	5.2	257	2	Q543Z4_MOUSE	Q543z4 mus musculus
900	167	5.3	633	2	Q8F3R6_LEPIN	Q8ay15 rattus norv	973	164	5.2	426	2	Q8F213_LEPIN	Q8f213 leptospira
901	167	5.3	743	2	Q84CF7_LISMO	Q8f3r6 leptospira	974	164	5.2	515	2	Q60MT7_CAEBR	Q60mt7 caenorhabdi
902	167	5.3	744	2	Q8KTF4_LISMO	Q84cf7 listeria mo	975	164	5.2	559	2	Q60UG7_CAEBR	Q60ug7 caenorhabdi
903	167	5.3	794	2	Q6YW99_ORYSA	Q8ktf4 listeria mo	976	164	5.2	570	2	Q8L3T8_ORYSA	Q8l3t8 oryza sativ
904	167	5.3	838	1	TLR4_CRIGR	Q6yw99 oryza sativ	977	164	5.2	611	2	Q7T062_MOUSE	Q7tq62 mus musculus
905	167	5.3	939	2	Q4SZU0_TETNG	Q9w82 cricetus	978	164	5.2	696	1	SLIK1_HUMAN	Q96px8 homo sapien
906	167	5.3	1112	2	Q41397_LYCPM	Q4szu0 tetraodon n	979	164	5.2	696	2	SLIK1_MOUSE	Q5u516 mus musculus
907	167	5.3	1112	2	Q41398_LYCPM	Q41397 lycopersico	980	164	5.2	696	2	Q5U516_HUMAN	Q5u516 homo sapien

981	164	5.2	696	2	Q5RAC4_PONPY	Q5rac4	pongo pygma	1054	161	5.1	1019	2	Q4RW99_TETNG	Q4rw99	tetraodon n
982	164	5.2	760	2	Q63Z70_MOUSE	Q63z70	mus musculus	1055	160.5	5.1	487	2	Q7QK12_ANOGA	Q7qk12	anopheles g
983	164	5.2	805	2	Q7QF00_ANOGA	Q7qf00	anopheles g	1056	160.5	5.1	519	1	AMGO2_MOUSE	Q80zd9	mus musculus
984	164	5.2	828	1	LGR6_HUMAN	Q9hbx8	homo sapien	1057	160.5	5.1	519	2	Q4VB86_MOUSE	Q4vbe6	mus musculus
985	164	5.2	833	2	Q7Q8I8_ANOGA	Q7q8i8	anopheles g	1058	160.5	5.1	664	2	Q5EWY7_CTEID	Q5ewy7	ctenopharyn
986	164	5.2	839	2	Q8MIQ2_RABIT	Q8miq2	oryctolagus	1059	160.5	5.1	1446	2	Q3V8Z0_DROME	Q3v8z0	ctenophylla
987	164	5.2	870	2	Q6PCD4_HUMAN	Q6pcd4	homo sapien	1060	160.5	5.1	2910	2	O55225_MOUSE	O55225	mus musculus
988	164	5.2	904	1	TLR3_HUMAN	O15455	homo sapien	1061	160.5	5.1	3889	2	Q6SS88_CHLRE	Q6sse8	chlamydomon
989	164	5.2	904	2	Q504W0_HUMAN	Q504w0	homo sapien	1062	160	5.1	258	2	Q4GLU6_EPTST	Q4glu6	eptatretus
990	164	5.2	904	2	Q4VAL2_HUMAN	Q4val2	homo sapien	1063	160	5.1	518	2	Q4R5R9_MACFA	Q4r5r9	macaca fasc
991	164	5.2	1032	2	Q865B9_CANFA	Q865b9	canis famil	1064	160	5.1	744	2	Q65375_ARATH	Q65375	arabidopsis
992	164	5.2	1395	2	Q7SC01_NEUCR	Q7sc01	neurospora	1065	160	5.1	950	2	Q5H723_FUGRU	Q5h723	fugu rubrip
993	164	5.2	1913	2	Q5SVA2_HUMAN	Q5sva2	homo sapien	1066	160	5.1	1050	2	Q3BN18_DROME	Q3bn18	drosohilla
994	164	5.2	2045	1	AGRN_HUMAN	O00468	homo sapien	1067	160	5.1	1080	2	Q69P46_ORYSA	Q69p46	oryza sativ
995	164	5.2	2045	2	Q60FE1_HUMAN	Q60fe1	homo sapien	1068	160	5.1	1096	2	Q8W556_ARATH	Q8w556	arabidopsis
996	163.5	5.2	163	2	Q6E410_PETMA	Q6e410	petromyzon	1069	160	5.1	1402	1	LAP2_MOUSE	Q80t82	mus musculus
997	163.5	5.2	166	2	Q6E4H7_PETMA	Q6e4h7	petromyzon	1070	160	5.1	1496	2	Q92626_HUMAN	Q92626	homo sapien
998	163.5	5.2	180	2	Q6A4H7_PETMA	Q6a4h7	petromyzon	1071	159.5	5.1	187	2	Q6E4I5_PETMA	Q6e4i5	petromyzon
999	163.5	5.2	362	2	Q502F2_BRARE	O502f2	brachydanio	1072	159.5	5.1	235	2	Q4G1I5_EPTST	Q4g1i5	eptatretus
1000	163.5	5.2	370	2	Q9DE04_ORENI	Q9de04	oreochromis	1073	159.5	5.1	412	2	Q5MIQ1_AEDAL	Q5miq1	aedes albop
1001	163.5	5.2	582	2	Q5R5R1_PONPY	Q5r5r1	pongo pygma	1074	159.5	5.1	494	2	Q9LHF1_ARATH	Q9lhf1	arabidopsis
1002	163.5	5.2	671	2	Q53GZ4_HUMAN	Q53gz4	homo sapien	1075	159.5	5.1	520	1	AMGO2_RAT	Q7tnj4	rattus norv
1003	163.5	5.2	786	2	Q48809_ARATH	O48809	arabidopsis	1076	159.5	5.1	636	2	Q8SQH3_CANFA	Q8sqh3	canis famil
1004	163	5.2	359	2	Q9DE03_ORENI	Q9de03	oreochromis	1077	159.5	5.1	722	2	Q4KMG2_HUMAN	Q4kmg2	homo sapien
1005	163	5.2	452	2	Q4RQB6_TETNG	Q4rqb6	tetraodon n	1078	159.5	5.1	1112	2	O64486_ARATH	O64486	arabidopsis
1006	163	5.2	501	2	Q6ZH85_ORYSA	Q6zh85	oryza sativ	1079	159	5.1	257	1	LRR3_RAT	P59035	rattus norv
1007	163	5.2	524	2	Q8R378_MOUSE	Q8r378	mus musculus	1080	159	5.1	524	1	LRR31_HUMAN	Q9bt6	homo sapien
1008	163	5.2	582	1	SHOC2_MOUSE	O88520	mus musculus	1081	159	5.1	524	2	O5TGN3_HUMAN	Q5tgn3	homo sapien
1009	163	5.2	929	2	Q6P9N3_MOUSE	Q6p9n3	mus musculus	1082	159	5.1	543	2	Q8S7M7_ORYSA	Q8s7m7	oryza sativ
1010	163	5.2	933	2	Q9BJD5_STRPU	Q9bjd5	strongyloce	1083	159	5.1	550	1	L612_MOUSE	Q8k4z0	mus musculus
1011	163	5.2	961	2	Q76CT7_PAROL	Q76ct7	paralichthy	1084	159	5.1	626	2	Q9NDD1_LEITR	Q9ndd1	leishmania
1012	163	5.2	961	2	Q76CT9_PAROL	Q76ct9	paralichthy	1085	159	5.1	671	2	Q60YZ3_CABBR	Q60yz3	caenorhabdi
1013	163	5.2	1221	2	Q9BIW9_CABEL	Q9biw9	caenorhabdi	1086	159	5.1	695	2	Q93539_CABEL	Q93539	caenorhabdi
1014	163	5.2	1612	1	LAP4_MOUSE	Q80u72	mus musculus	1087	159	5.1	964	1	Q86U22_HUMAN	Q86u22	homo sapien
1015	162.5	5.2	283	2	Q9V428_DROME	Q9v428	drosohilla	1088	159	5.1	984	1	RIN3_HUMAN	RIN3	homo sapien
1016	162.5	5.2	375	2	O5XIH1_RAT	O5xih1	rattus norv	1089	159	5.1	985	2	Q76LE3_HUMAN	Q76le3	homo sapien
1017	162.5	5.2	452	2	Q8F118_LEPIN	Q8f118	leptospira	1090	159	5.1	1119	2	Q8Z0H2_ANASP	Q8z0h2	anabaena sp
1018	162.5	5.2	494	2	Q9VEK6_DROME	Q9veke	drosohilla	1091	158.5	5.1	163	2	Q6E4B4_PETMA	Q6e4b4	petromyzon
1019	162.5	5.2	527	2	Q6EPB5_DROME	Q6epb5	drosohilla	1092	158.5	5.1	166	2	Q6E4B6_PETMA	Q6e4b6	petromyzon
1020	162.5	5.2	641	2	Q8MQM0_DROME	Q8mqm0	drosohilla	1093	158.5	5.1	242	2	Q4SSH2_TETNG	Q4ssh2	tetraodon n
1021	162.5	5.2	700	2	Q4R6H5_MACFA	Q4r6h5	macaca fasc	1094	158.5	5.1	371	2	Q4T5R8_TETNG	Q4t5r8	tetraodon n
1022	162.5	5.2	1045	2	Q5H717_FUGRU	Q5h717	fugu rubrip	1095	158.5	5.1	417	2	O15828_LEICH	O15828	leishmania
1023	162	5.2	234	2	Q4G1H3_EPTST	Q4g1h3	eptatretus	1096	158.5	5.1	656	2	Q19312_CABEL	Q19312	caenorhabdi
1024	162	5.2	242	2	Q9UG10_HUMAN	Q9ug10	homo sapien	1097	158.5	5.1	738	2	Q33373_CABEL	Q33373	caenorhabdi
1025	162	5.2	375	2	Q7Q118_ANOGA	Q7q118	anopheles g	1098	158.5	5.1	943	2	Q4S133_TETNG	Q4s133	tetraodon n
1026	162	5.2	613	2	Q7Z5L7_HUMAN	Q7z5l7	homo sapien	1099	158.5	5.1	953	2	Q9V701_DROME	Q9v701	drosohilla
1027	162	5.2	642	2	Q6UXL8_HUMAN	Q6uxl8	homo sapien	1100	158.5	5.1	1007	2	Q8MQU9_AEDAE	Q8mqu9	aedes aegyp
1028	162	5.2	642	2	Q5VVZ2_HUMAN	O5vvz2	homo sapien	1101	158.5	5.1	1032	1	TLR8_MOUSE	P58682	mus musculus
1029	162	5.2	649	2	O8C2M4_MOUSE	O8c2m4	homo sapien	1102	158.5	5.1	1061	2	Q655V6_ORYSA	Q655v6	oryza sativ
1030	162	5.2	661	2	Q6FIR3_HUMAN	Q6fir3	homo sapien	1103	158.5	5.1	1123	2	Q65XS7_ORYSA	Q65xs7	oryza sativ
1031	162	5.2	661	2	Q5VVZ3_HUMAN	Q5vvz3	homo sapien	1109	158	5.0	317	2	Q7Z235_BRARE	Q7zz35	brachydanio
1032	162	5.2	942	2	Q7Q1S8_ANOGA	Q7q1s8	anopheles g	1104	158.5	5.1	1181	2	O72235_BRARE	O72235	brachydanio
1033	162	5.2	1040	2	Q6Z8Y3_ORYSA	Q6z8y3	oryza sativ	1111	158	5.0	377	2	Q72U33_LEPIC	Q72u33	leptospira
1034	161.5	5.2	259	2	Q7QHK8_ANOGA	Q7qhk8	anopheles g	1112	158	5.0	510	2	Q9NIR8_DICDI	Q9nir8	dictyosteli
1035	161.5	5.2	268	2	Q4KP17_9PETR	Q4kp17	ichthyomyzo	1106	158.5	5.1	1300	2	Q9NKD6_DROME	Q9nkd6	drosohilla
1036	161.5	5.2	351	2	Q5T500_XENLA	Q5t500	xenopus lae	1107	158	5.0	239	2	Q4KP19_9PETR	Q4kp19	ichthyomyzo
1037	161.5	5.2	507	2	Q9N3F2_CABEL	Q9n3f2	caenorhabdi	1108	158	5.0	249	2	Q4KP07_LAMAP	Q4kp07	lampetra ap
1038	161.5	5.2	519	2	Q7Q116_ANOGA	Q7q116	anopheles g	1110	158	5.0	352	1	Q96B32_HUMAN	Q96b32	homo sapien
1039	161.5	5.2	841	1	TLR4_BOVIN	Q9g165	bos taurus	1111	158	5.0	510	2	KERA_HUMAN	O60938	homo sapien
1040	161.5	5.2	841	2	Q6WCD4_BOVIN	Q6wcd4	bos taurus	1113	158	5.0	531	2	O5TW51_ANOGA	O5tw51	anopheles g
1041	161.5	5.2	841	2	Q6WCD5_BOVIN	Q6wcd5	bos taurus	1114	158	5.0	677	2	O5XPY7_1CTPU	O5xpy7	ictalurus p
1042	161.5	5.2	841	2	Q8SQ55_BOVIN	Q8sq55	bos taurus	1115	158	5.0	741	2	Q9VJA9_DROME	Q9vja9	drosohilla
1043	161.5	5.2	1193	2	Q4SL20_TETNG	Q4sl20	tetraodon n	1116	158	5.0	838	2	Q4SWS3_TETNG	Q4sws3	tetraodon n
1044	161.5	5.2	1270	2	Q5RKS1_RAT	Q5rks1	rattus norv	1117	158	5.0	879	2	Q68CI3_ONCMY	Q68ci3	oncorhynch
1045	161	5.1	557	2	Q7QF88_ANOGA	Q7qf88	anopheles g	1118	158	5.0	909	2	Q5ZRC2_HUMAN	Q5zrc2	homo sapien
1046	161	5.1	598	2	Q6MP66_CABEL	Q6mp66	caenorhabdi	1119	158	5.0	1032	2	O56R09_AOTNA	O56r09	aotus nancy
1047	161	5.1	559	2	Q22875_CABEL	Q22875	caenorhabdi	1120	158	5.0	5703	1	MUC5B_HUMAN	Q9hcr4	homo sapien
1048	161	5.1	586	2	Q93377_CABEL	Q93377	caenorhabdi	1121	157.5	5.0	163	2	Q6E4I4_PETMA	Q6e4i4	petromyzon
1049	161	5.1	682	1	CONN_DROME	O01819	drosohilla	1122	157.5	5.0	224	2	Q9DE01_BRARE	Q9de01	brachydanio
1050	161	5.1	691	2	Q6AWM0_DROME	Q6awm0	drosohilla	1123	157.5	5.0	272	2	Q7KWF0_DROME	Q7kwf0	drosohilla
1051	161	5.1	861	2	Q9SLS3_TOBAC	Q9sls3	nicotiana t	1124	157.5	5.0	276	2	Q7PSP4_ANOGA	Q7psp4	anopheles g
1052	161	5.1	905	2	Q7TNI8_RAT	Q7tni8	rattus norv	1125	157.5	5.0	396	2	O5DZ80_VIBF1	O5dz80	vibrio fisc
1053	161	5.1	945	2	Q801F9_CARAU	Q801f9	carassius a	1126	157.5	5.0	655	2	Q4RW74_TETNG	Q4rw74	tetraodon n

1127 157.5 5.0 861 2 Q50TQ5_ENTHI Q50tcq5 entamoeba h 1200 154.5 4.9 2461 2 Q56D06_HUMAN Q56d06 homo sapien
 1128 157.5 5.0 1102 2 Q4RZY0_TETNG Q4rzy0 tetradon n 1201 154.5 4.9 2517 1 NCOR2_HUMAN NCOR2 h nuclear r
 1129 157.5 5.0 2657 2 Q4S189_TETNG Q4s189 tetradon n 1202 154 4.9 399 2 Q8STX6_ENCCU Q8stx6 encephalito
 1130 157 5.0 266 2 Q7Q1P7_ANOGA Q7q1p7 anopheles g 1203 154 4.9 458 2 Q9VU13_DROME Q9vul13 drosophila
 1131 157 5.0 273 2 Q9NUU4_HUMAN Q9nuu4 homo sapien 1204 154 4.9 491 2 Q6KAP0_MOUSE Q6kap0 mus musculus
 1132 157 5.0 377 2 Q8F119_LEPIN Q8f119 leptospira 1205 154 4.9 530 2 P97830_RAT P97830 rattus norv
 1133 157 5.0 444 2 Q9H5H8_HUMAN Q9h5h8 homo sapien 1206 154 4.9 584 2 Q49751_ARATH Q49751 arabidopsis
 1134 157 5.0 592 2 Q7L236_HUMAN Q7l236 homo sapien 1207 154 4.9 584 2 Q8L722_ARATH Q8l722 arabidopsis
 1135 157 5.0 613 2 Q940B8_MAIZE Q940b8 zea mays (m 1208 154 4.9 812 2 Q9VFY9_DROME Q9vfy9 drosophila
 1136 157 5.0 622 2 Q8N3B0_HUMAN Q8n3b0 homo sapien 1209 154 4.9 825 2 Q63U08_BURPS Q63u08 burkholderi
 1137 157 5.0 680 1 LRCH4_MOUSE Q921g6 mus musculus 1210 154 4.9 953 2 Q8VVG7_ARATH Q8vvg7 arabidopsis
 1138 157 5.0 796 2 Q8NSJ5_HUMAN Q8nsj5 homo sapien 1211 154 4.9 965 2 Q5H724_FUGRU Q5h724 fugu rubrip
 1139 157 5.0 903 2 Q6IWI5_BRARE Q6iwi5 brachydanio 1212 154 4.9 1845 2 Q80UA8_MOUSE Q80ua8 mus musculus
 1140 157 5.0 1032 2 Q5I2M6_RAT Q5i2m6 rattus norv 1213 153.5 4.9 163 2 Q6E4L8_PETMA Q6e4l8 petromyzon
 1141 157 5.0 1032 2 Q6Y180_RAT Q6y180 rattus norv 1214 153.5 4.9 166 2 Q6E4G9_PETMA Q6e4g9 petromyzon
 1142 156.5 5.0 305 2 Q50QO5_ENTHI Q50qo5 entamoeba h 1215 153.5 4.9 246 2 Q4KP02_LAMAP Q4kp02 lampetra ap
 1143 156.5 5.0 360 1 PGS2_RABIT Q82888 oryctolagus 1216 153.5 4.9 366 2 Q5R858_PONPY Q5r858 pongo pygma
 1144 156.5 5.0 376 1 PNOD_HUMAN Q66828 homo sapien 1217 153.5 4.9 389 2 Q4RHN9_TETNG Q4rhn9 tetradon n
 1145 156.5 5.0 428 2 Q9VDD4_DROME Q9vdd4 drosophila 1218 153.5 4.9 403 2 Q96CX6_HUMAN Q96cx6 homo sapien
 1146 156.5 5.0 487 2 Q7Q087_ANOGA Q7q087 anopheles g 1219 153.5 4.9 526 2 Q5BLJ6_BRARE Q5blj6 brachydanio
 1147 156.5 5.0 505 2 Q4RV89_TETNG Q4rv89 tetradon n 1220 153.5 4.9 655 2 Q9FBR7_STRCO Q9fbr7 streptomyce
 1148 156.5 5.0 524 2 Q6AXP5_RAT Q6axp5 rattus norv 1221 153.5 4.9 685 2 Q72TH0_LEPIC Q72th0 leptospira
 1149 156.5 5.0 551 2 Q5ZB68_ORYSA Q5zb68 oryza sativ 1222 153.5 4.9 685 2 Q8F1V0_LEPIN Q8f1v0 leptospira
 1150 156.5 5.0 711 2 Q9SPW1_LXCES Q9spw1 lycopersico 1223 153.5 4.9 802 2 Q8L4U4_ORYSA Q8l4u4 oryza sativ
 1151 156.5 5.0 887 1 UFO_HUMAN P30530 homo sapien 1224 153.5 4.9 864 2 Q8LPG4_ARATH Q8lpg4 arabidopsis
 1152 156.5 5.0 980 2 Q9ZU10_ARATH Q9zu10 arabidopsis 1225 153.5 4.9 864 2 Q9T033_ARATH Q9t033 arabidopsis
 1153 156.5 5.0 1179 2 Q7PMD3_ANOGA Q7pmd3 anopheles g 1226 153.5 4.9 894 2 Q8N5L2_HUMAN Q8n5l2 homo sapien
 1154 156.5 5.0 1301 2 Q9VZ81_DROME Q9vz81 drosophila 1227 153.5 4.9 940 2 Q4RGH3_TETNG Q4rgh3 tetradon n
 1155 156.5 5.0 1766 2 Q6XHA8_DICDI Q6xha8 dictyosteli 1228 153.5 4.9 987 2 Q53MD2_ORYSA Q53md2 oryza sativ
 1156 156.5 5.0 1867 2 Q54M77_DICDI Q54m77 dictyosteli 1229 153.5 4.9 1032 1 TLR9_HUMAN TLR9 mus muscu
 1157 156 5.0 163 2 Q6E4D2_PETMA Q6e4d2 petromyzon 1230 153.5 4.9 1041 2 Q9FI15_ARATH Q9fi15 arabidopsis
 1158 156 5.0 163 2 Q6E4F5_PETMA Q6e4f5 petromyzon 1231 153.5 4.9 1110 2 Q9FI77_ARATH Q9fi77 arabidopsis
 1159 156 5.0 257 1 LARC3_HUMAN Q9by71 rattus norv 1232 153.5 4.9 1121 2 Q942P3_ORYSA Q942p3 oryza sativ
 1160 156 5.0 354 1 PGS2_RAT Q91129 rattus norv 1233 153.5 4.9 1388 2 Q4RIV6_TETNG Q4riv6 tetradon n
 1161 156 5.0 422 2 Q4RH13_TETNG Q4rh13 tetradon n 1234 153.5 4.9 3247 2 Q65553_9ALPH Q65553 9alphe
 1162 156 5.0 449 2 Q9W128_DROME Q9w128 drosophila 1235 153.5 4.9 3247 2 Q77CD4_9ALPH Q77cd4 9alphe
 1163 156 5.0 547 2 Q4QG16_LEIMA Q4qg16 leishmania 1236 153 4.9 367 2 Q6GLE8_XENTR Q6gle8 xenotr
 1164 156 5.0 552 2 Q8K375_MOUSE Q8k375 mus musculus 1237 153 4.9 529 2 Q5F4C4_CHICK Q5f4c4 gallus gall
 1165 156 5.0 575 2 Q571F2_MOUSE Q571f2 mus musculus 1238 153 4.9 548 2 Q4V8C9_RAT Q4v8c9 rattus norv
 1166 156 5.0 594 2 Q9U3A0_CABEL Q9u3a0 caenorhabdi 1239 153 4.9 581 2 Q9DSQ5_MOUSE Q9dsq5 m mus muscu
 1167 156 5.0 643 2 Q6Q148_RAT Q6q148 rattus norv 1240 153 4.9 590 2 Q9D2F4_MOUSE Q9d2f4 m mus muscu
 1168 156 5.0 704 2 Q4QGK1_LEIMA Q4qgk1 leishmania 1241 153 4.9 699 1 VGLG_HV2H VGLG human herpe
 1169 156 5.0 940 2 Q8T753_BRAFL Q8t753 brachiosteo 1242 153 4.9 720 2 Q6PQA5_SPAAU Q6pqa5 sparus auri
 1170 156 5.0 953 2 Q61709_CABER Q61709 caenorhabdi 1243 153 4.9 1840 2 Q9ULI4_HUMAN Q9uli4 homo sapien
 1171 156 5.0 1039 2 Q86B11_DROME Q86b11 drosophila 1244 153 4.9 2042 1 MDC1_PIG MDC1 petromyzon
 1172 155.5 5.0 332 2 Q6C2U8_YARLI Q6c2u8 varrowia li 1245 152.5 4.9 163 2 Q6E4F3_PETMA Q6e4f3 petromyzon
 1173 155.5 5.0 338 2 Q6YEX8_CHICK Q6yex8 gallus gall 1246 152.5 4.9 370 2 Q5R9V7_PONPY Q5r9v7 pongo pygma
 1174 155.5 5.0 367 2 Q8BK43_MOUSE Q8bk43 mus musculus 1247 152.5 4.9 372 2 Q5VZS8_HUMAN Q5vzs8 homo sapien
 1175 155.5 5.0 664 2 Q5EWY6_CTEID Q5ewy6 ctenopharyn 1248 152.5 4.9 550 2 Q7PT66_ANOGA Q7pt66 anopheles g
 1176 155.5 5.0 980 2 Q80WA0_MOUSE Q80wa0 mus musculus 1249 152.5 4.9 577 2 Q8AVI4_XENLA Q8avi4 xenopus lae
 1177 155.5 5.0 1102 2 Q8KC98_CHLTE Q8kc98 chlorobium 1250 152.5 4.9 581 2 Q9AN90_BRAJA Q9an90 bradyrhizob
 1178 155.5 5.0 1135 2 Q84RP6_ARATH Q84rp6 arabidopsis 1251 152.5 4.9 585 2 Q89TL5_BRAJA Q89tl5 bradyrhizob
 1179 155.5 5.0 1285 1 CRUM2_HUMAN Q5i148 homo sapien 1252 152.5 4.9 849 1 LAP1_DROME LAP1 drosophila
 1180 155.5 5.0 1334 2 Q9RKR9_STRCO Q9rkr9 streptomyce 1253 152.5 4.9 1047 2 Q5H719_FUGRU Q5h719 fugu rubrip
 1181 155 4.9 347 2 Q9DE00_PETMA Q9de00 petromyzon 1254 152.5 4.9 1109 2 Q8H4J0_ORYSA Q8h4j0 oryza sativ
 1182 155 4.9 504 1 AMGO3_HUMAN Q86kw7 homo sapien 1255 152.5 4.9 1287 2 Q5TMV4_ANOGA Q5tmv4 anopheles g
 1183 155 4.9 576 2 Q6Z8P4_ORYSA Q6z8p4 oryza sativ 1256 152.5 4.9 1295 2 Q8T0X1_BOMMO Q8t0x1 bombyx mori
 1184 155 4.9 719 2 Q8VJQ6_WYCTU Q8vjq6 mycobacteri 1257 152.5 4.9 1356 2 Q8WRE2_ANOGA Q8wre2 anopheles g
 1185 155 4.9 825 2 Q82JU8_BURMA Q82ju8 burkholderi 1258 152.5 4.9 1817 2 Q4WMC5_ASPPFO Q4wmc5 aspergillus
 1186 155 4.9 961 2 P90920_CABEL Q9n97 homo sapien 1259 152.5 4.9 3288 2 Q7TSD9_CHV1 Q7t5d9 cercopithe
 1187 155 4.9 1041 1 TLR8_HUMAN Q9n97 homo sapien 1260 152 4.8 443 1 LRC17_MOUSE LRC17 mus muscu
 1188 154.5 4.9 219 2 Q90WZ2_CHICK Q90wz2 gallus gall 1261 152 4.8 562 2 Q5JN60_ORYSA Q5jn60 oryza sativ
 1189 154.5 4.9 246 2 Q4KP18_9PETR Q4kp18 ichtthyomyzo 1262 152 4.8 682 2 Q5JN60_ORYSA Q5jn60 oryza sativ
 1190 154.5 4.9 376 2 Q8IV47_HUMAN Q8iv47 homo sapien 1263 152 4.8 776 2 Q6R2K3_ARATH Q6r2k3 arabidopsis
 1191 154.5 4.9 524 1 LRCR3_MOUSE Q8ovq1 mus musculus 1264 152 4.8 786 1 TLR1_HUMAN TLR1 homo sapien
 1192 154.5 4.9 548 2 Q9VJU1_DROME Q9vjul drosophila 1265 152 4.8 786 2 Q6FI64_HUMAN Q6fi64 homo sapien
 1193 154.5 4.9 601 2 Q571M3_MOUSE Q571m3 mus musculus 1266 152 4.8 786 2 Q5FWG5_HUMAN Q5fwg5 homo sapien
 1194 154.5 4.9 631 2 Q8TN14_METAC Q8tn14 methanosarc 1267 152 4.8 796 1 TLR6_HUMAN TLR6 homo sapien
 1195 154.5 4.9 1013 2 Q9M0G7_ARATH Q9m0g7 arabidopsis 1268 152 4.8 863 2 Q4R6F0_MACFA Q4r6f0 macaca fasc
 1196 154.5 4.9 1109 2 Q6YT77_ORYSA Q6yt77 oryza sativ 1269 151.5 4.8 347 2 Q9D9Q0_MOUSE Q9d9q0 mus musculus
 1197 154.5 4.9 1143 2 Q9SUB9_ARATH Q9sub9 arabidopsis 1270 151.5 4.8 507 2 Q61X12_CAEBR Q61x12 caenorhabdi
 1198 154.5 4.9 1192 1 EXS_ARATH Q91yn8 arabidopsis 1271 151.5 4.8 623 2 Q7Q090_ANOGA Q7q090 anopheles g
 1199 154.5 4.9 1961 2 Q6MG89_RAT Q6mg89 rattus norv 1272 151.5 4.8 710 2 Q5TR39_ANOGA Q5tr39 anopheles g

1273	151.5	4.8	855	2	Q8L3Y5 SOYBN	Q8L3Y5 glycine max
1274	151.5	4.8	997	2	Q6K7X5 ORYSA	Q6K7X5 oryza sativ
1275	151.5	4.8	998	2	Q4W9M1 ASPFU	Q4w9m1 aspergillus
1276	151.5	4.8	1109	2	Q4WZJ8 ORYSA	Q4wzj8 oryza sativ
1277	151.5	4.8	1152	2	Q7PFC4 ANOGA	Q7pfc4 anopheles g
1278	151.5	4.8	1152	2	Q8WRES ANOGA	Q8wres anopheles g
1279	151.5	4.8	1775	2	Q4S4S11 DICDI	Q4s4s11 dictyosteli
1280	151	4.8	163	2	Q6E4H9 PETMA	Q6e4h9 petromyzon
1281	151	4.8	399	2	Q8BM45 MOUSE	Q8bm45 m mus muscu
1282	151	4.8	508	2	Q5OZ7F6 ENTHI	Q5oz7f6 entamoeba h
1283	151	4.8	530	2	Q8R934 MOUSE	Q8r934 mus musculu
1284	151	4.8	540	2	Q6V6S6 DROSI	Q6v6s6 drosophila
1285	151	4.8	540	2	P93666 HELAN	P93666 helianthus
1286	151	4.8	541	2	Q6V6S8 DROSI	Q6v6s8 drosophila
1287	151	4.8	541	2	Q6V6S9 DROSI	Q6v6s9 drosophila
1288	151	4.8	541	2	Q6V6T0 DROSI	Q6v6t0 drosophila
1289	151	4.8	581	2	Q04143 SILLA	Q04143 silene lati
1290	151	4.8	784	2	Q6YGU2 RAT	Q6ygu2 rattus norv
1291	151	4.8	793	2	Q704V6 BOVIN	Q704v6 bos taurus
1292	151	4.8	793	2	Q706D2 BOVIN	Q706d2 bos taurus
1293	151	4.8	835	1	TLR4_MOUSE	Tlr4 mouse
1294	151	4.8	835	2	Q5RG74 MOUSE	Q5rg74 mus musculu
1295	151	4.8	947	2	Q8RUT5 ORYSA	Q8rut5 oryza sativ
1296	151	4.8	1030	2	Q8H037 ORYSA	Q8h037 oryza sativ
1297	151	4.8	1385	2	Q9V8Z5 DROME	Q9v8z5 drosophila
1298	151	4.8	1389	2	Q24591 DROME	Q24591 drosophila
1299	150.5	4.8	289	2	Q8F3F4 LEPIN	Q8f3f4 leptospira
1300	150.5	4.8	329	2	Q8F115 LEPIN	Q8f115 leptospira
1301	150.5	4.8	408	2	Q8F212 LEPIN	Q8f212 leptospira
1302	150.5	4.8	413	2	Q72TC4 LEPIC	Q72tc4 leptospira
1303	150.5	4.8	423	1	OMD RAT	Q9c1s67 rattus norv
1304	150.5	4.8	537	2	Q9C769 ARATH	Q9c769 arabidopsis
1305	150.5	4.8	641	2	Q4TBJ8 TETNG	Q4tcbj8 tetraodon n
1306	150.5	4.8	648	2	Q8BU93 MOUSE	Q8bu93 m mus muscu
1307	150.5	4.8	685	2	Q6AXU3 BRARE	Q6axl3 brachydanio
1308	150.5	4.8	695	1	F8HR HUMAN	P23945 homo sapien
1309	150.5	4.8	695	2	Q4QRJ3 HUMAN	Q4qrj3 homo sapien
1310	150.5	4.8	818	2	Q76CTU PAROL	Q76ctu paralichthy
1311	150.5	4.8	871	2	Q5H726 FUGRU	Q5h726 fugu rubrip
1312	150.5	4.8	1107	2	Q8BKp3 MOUSE	Q8bkp3 m mus muscu
1313	150.5	4.8	1109	1	RPK1_IPONI	P93194 ipomoea nil
1314	150.5	4.8	1140	2	Q1RL04 ARATH	Q1rlr04 arabidopsis
1315	150.5	4.8	1149	2	Q6GQR9 MOUSE	Q6gqr9 mus musculu
1316	150.5	4.8	1461	2	Q94H87 ORYSA	Q94h87 oryza sativ
1317	150.5	4.8	1702	2	Q7PS39 ANOGA	Q7ps39 anopheles g
1318	150.5	4.8	1898	2	Q6ZP14 MOUSE	Q6zp14 mus musculu
1319	150.5	4.8	1944	2	Q4S1G7 TETNG	Q4s1g7 tetraodon n
1320	150	4.8	163	2	Q6E4E8 PETMA	Q6e4e8 petromyzon
1321	150	4.8	239	2	Q4KP08 LAMAP	Q4kp08 lampetra ap
1322	150	4.8	259	1	L3C3B_HUMAN	Q9c6b8 homo sapien
1323	150	4.8	259	1	L3C3B_MOUSE	Q9c6b8 mus musculu
1324	150	4.8	259	2	Q5M8T0 HUMAN	Q5m8t0 homo sapien
1325	150	4.8	259	2	Q543Z7 MOUSE	Q543z7 mus musculu
1326	150	4.8	272	1	P9S1_PIG	Q9c6q6 sus scrofa
1327	150	4.8	305	2	Q9N028 MACFA	Q9n028 macaca fasc
1328	150	4.8	342	2	Q4V9E0 BRARE	Q4v9e0 brachydanio
1329	150	4.8	348	2	Q756S8 ASHGO	Q756s8 ashbysa goss
1330	150	4.8	367	2	Q86X40 HUMAN	Q86x40 homo sapien
1331	150	4.8	584	2	Q49750 ARATH	Q49750 arabidopsis
1332	150	4.8	594	2	Q4SDI8 TETNG	Q4sdi8 tetraodon n
1333	150	4.8	652	2	Q8QUM9 ARATH	Q8qum9 arabidopsis
1334	150	4.8	796	2	Q59H16_PIG	Q59h16 sus scrofa
1335	150	4.8	796	2	Q76L23_PIG	Q76l23 sus scrofa
1336	150	4.8	802	2	Q8LFN2 ARATH	Q8lfn2 arabidopsis
1337	150	4.8	803	2	Q9SRV4 ARATH	Q9srv4 arabidopsis
1338	150	4.8	1294	2	Q8RZV7 ORYSA	Q8rzv7 oryza sativ
1339	150	4.8	1305	1	TCGAP_MOUSE	Q8gyf9 mus musculu
1340	150	4.8	1315	1	CHAO_DROME	P12024 drosophila
1341	149.5	4.8	98	2	Q90XG3_CHICK	Q90xg3 gallus gall
1342	149.5	4.8	163	2	Q6E4E9 PETMA	Q6e4e9 petromyzon
1343	149.5	4.8	164	2	Q6E4G8 PETMA	Q6e4g8 petromyzon
1344	149.5	4.8	167	2	Q6E4I1 PETMA	Q6e4i1 petromyzon
1345	149.5	4.8	224	2	Q44086_CABEL	Q44086 caenorhabdi

1346	149.5	4.8	542	2	Q6V4C6 DROYA	Q6v4c6 drosophila
1347	149.5	4.8	657	2	Q6L569 ORYSA	Q6l569 oryza sativ
1348	149.5	4.8	696	2	Q8DGF5_CYNPY	Q8dgs5 cynops pyrr
1349	149.5	4.8	894	2	Q8GYN8 ARATH	Q8gyr8 arabidopsis
1350	149.5	4.8	957	2	Q7SR12 ARATH	Q7sr12 arabidopsis
1351	149.5	4.8	1056	2	Q7XFM6 ORYSA	Q7xfm6 oryza sativ
1352	149.5	4.8	1056	2	Q8S7A6 ORYSA	Q8s7a6 oryza sativ
1353	149.5	4.8	1469	2	Q51AW9_ENTHI	Q51aw9 entamoeba h
1354	149.5	4.8	1791	2	Q4P4A9_USTMA	Q4p4a9 ustiliago ma
1355	149	4.8	167	2	Q6E4D3_PETMA	Q6e4d3 petromyzon
1356	149	4.8	295	2	Q86DD0_CABEL	Q86dd0 caenorhabdi
1357	149	4.8	310	2	Q86S81_CAEEL	Q86s81 caenorhabdi
1358	149	4.8	341	2	Q9NSD7_CAEEL	Q9nsd7 caenorhabdi
1359	149	4.8	366	2	Q7QH02_ANOGA	Q7qh02 anopheles g
1360	149	4.8	375	2	Q9N4Z5_CAEEL	Q9n4z5 caenorhabdi
1361	149	4.8	421	2	Q7PNU0_ANOGA	Q7pnu0 anopheles g
1362	149	4.8	437	2	Q7Q6S9 ANOGA	Q7q6s9 anopheles g
1363	149	4.8	471	2	Q9LRV8 ARATH	Q9lrsv8 arabidopsis
1364	149	4.8	763	2	Q4Q5O5_LEIMA	Q4q5o5 leishmania
1365	149	4.8	784	1	TLR2_CRIGR	Q9rlf8 cricetulus
1366	149	4.8	927	2	Q8N537_HUMAN	Q8n537 homo sapien
1367	149	4.8	972	2	Q5AXH5_EMENI	Q5axh5 aspergillus
1368	149	4.8	1025	2	Q40640 ORYSA	Q40640 oryza sativ
1369	149	4.8	1025	2	Q7DMC2_ORYLO	Q7dmc2 oryza longi
1370	149	4.8	1143	1	BRL2_ARATH	Q9zps9 arabidopsis
1371	149	4.8	1164	2	Q53JZ9 ORYSA	Q53jz9 oryza sativ
1372	149	4.8	1504	2	Q9UES6_HUMAN	Q9ues6 homo sapien
1373	149	4.8	1504	2	Q6PIB4_HUMAN	Q6pib4 homo sapien
1374	149	4.8	1504	2	Q7ZZX6_HUMAN	Q7zzx6 homo sapien
1375	149	4.8	1504	2	Q6PGP3_HUMAN	Q6pgp3 homo sapien
1376	149	4.8	1522	2	O15069_HUMAN	O15069 homo sapien
1377	149	4.8	1528	2	Q9Y2I1_HUMAN	Q9y2i1 homo sapien
1378	149	4.8	1874	2	Q75F93_ASHGO	Q75f93 ashbysa goss
1379	149	4.8	2357	2	Q869S1_DICDI	Q869s1 dictyosteli
1380	149	4.8	2357	2	Q9UIM8_DICDI	Q9ulm8 dictyosteli
1381	148.5	4.7	163	2	Q6E4F7_PETMA	Q6e4f7 petromyzon
1382	148.5	4.7	215	2	Q91VH8_MOUSE	Q91vh8 mus musculu
1383	148.5	4.7	232	2	Q5T508_HUMAN	Q5t508 homo sapien
1384	148.5	4.7	321	2	Q6X8P9_BOVIN	Q6x8p9 bos taurus
1385	148.5	4.7	375	1	FMOD_BOVIN	P13605 bos taurus
1386	148.5	4.7	376	1	FMOD_RAT	P50609 rattus norv
1387	148.5	4.7	516	2	Q4T9I8_TETNG	Q4t9i8 tetraodon n
1388	148.5	4.7	610	2	Q21604_CAEEL	Q21604 caenorhabdi
1389	148.5	4.7	646	2	Q8PQD3_XANAC	Q8pqd3 xanthomonas
1390	148.5	4.7	680	2	Q93374_CAEEL	Q93374 caenorhabdi
1391	148.5	4.7	687	2	Q61PG2_CABER	Q61pg2 caenorhabdi
1392	148.5	4.7	695	1	FSHR_MACFA	P32212 macaca fasc
1393	148.5	4.7	807	2	Q6GPJ8_XENLA	Q6gpj8 xenopus lae
1394	148.5	4.7	890	2	Q9LQ11_ARATH	Q9lq11 arabidopsis
1395	148.5	4.7	964	2	Q8VVT7_ARATH	Q8vvt7 arabidopsis
1396	148.5	4.7	964	2	Q9LY03_ARATH	Q9ly03 arabidopsis
1397	148.5	4.7	1013	2	Q96PY9_HUMAN	Q96py9 homo sapien
1398	148.5	4.7	1016	2	Q9LRT1_ARATH	Q9lrt1 arabidopsis
1399	148.5	4.7	1099	2	Q8WXE4_HUMAN	Q8wx4 homo sapien
1400	148.5	4.7	1115	1	GR101_LYMYST	P46023 lymaea sta
1401	148.5	4.7	1140	2	Q7S718_NEUCR	Q7s718 neuropeora
1402	148.5	4.7	1279	2	Q4RJ85_TETNG	Q4rj85 tetraodon n
1403	148	4.7	311	2	Q8F116_LEPIN	Q8f116 leptospira
1404	148	4.7	338	1	LUM_RAT	P51886 rattus norv
1405	148	4.7	449	2	Q4SR98_TETNG	Q4sr98 tetraodon n
1406	148	4.7	572	2	Q72S79_LEPIC	Q72s79 leptospira
1407	148	4.7	581	2	Q505F5_MOUSE	Q505f5 mus musculu
1408	148	4.7	592	2	Q4REH6_TETNG	Q4ref6 tetraodon n
1409	148	4.7	724	2	Q651V0_ORYSA	Q651v0 oryza sativ
1410	148	4.7	745	2	Q89X06_BRAJA	Q89x06 bradyrhizob
1411	148	4.7	811	2	Q59HI5_PIG	Q59hi5 sus scrofa
1412	148	4.7	811	2	Q4LDR6_PIG	Q4ldr6 sus scrofa
1413	148	4.7	915	2	Q5SMW5_ORYSA	Q5smw5 oryza sativ
1414	148	4.7	1095	2	Q6URA2_BROSA	Q6ura2 malus bacca
1415	148	4.7	1188	2	Q41805_WAIZE	Q41805 zea mays (m
1416	148	4.7	1964	1	NOTC4_MOUSE	P31695 mus musculu
1417	148	4.7	2143	2	Q75T35_GIOLA	Q75t35 glomerella
1418	147.5	4.7	163	2	Q6E4M8_PETMA	Q6e4m8 petromyzon

QY	1	MCSRVPLLLPLLLLLALGFGVQCSPGSCQSQPQTVECTARQGTTPVRDVPDPPTVGLYVF	60
Db	1	MCSRVPLLLPLLLLLALGFGVQCSPGSCQSQPQTVECTARQGTTPVRDVPDPPTVGLYVF	60
QY	61	ENGIITWLDASSFAGLPGQLDLSONQITASLRPLRLDLSSNSLLALEPGLDITANVE	120
Db	61	ENGIITWLDASSFAGLPGQLDLSONQITASLRPLRLDLSSNSLLALEPGLDITANVE	120
QY	121	ALRLAGLGLQQLDEGLFSLRNLNLDVSDNQLSERVPVIRGLRGLTRLRLAGNTRIAQL	180
Db	121	ALRLAGLGLQQLDEGLFSLRNLNLDVSDNQLSERVPVIRGLRGLTRLRLAGNTRIAQL	180
QY	181	RPEDLAGLAALQELDVSNLSLQALPGDLGSLFPRRLRLAARNPFCVCPLSWFGPWRE	240
Db	181	RPEDLAGLAALQELDVSNLSLQALPGDLGSLFPRRLRLAARNPFCVCPLSWFGPWRE	240
QY	241	SHVTLASPEETRCHPPKNAGRLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL	300
Db	241	SHVTLASPEETRCHPPKNAGRLLELDYADFGCPATTTATVPTTRPVVREPTALSSSL	300
QY	301	APTWLSPATAPATEAPSPSTAPTVGPVPOQDCPSTCLNGGTCHLGTRHHLACLCPSG	360
Db	301	APTWLSPATAPATEAPSPSTAPTVGPVPOQDCPSTCLNGGTCHLGTRHHLACLCPSG	360
QY	361	FTGLYCESQMGQGTSPSTPTVTPRPSRLTLGIEPVSPTSLRVGLQRYLQGSVQLRSUR	420
Db	361	FTGLYCESQMGQGTSPSTPTVTPRPSRLTLGIEPVSPTSLRVGLQRYLQGSVQLRSUR	420
QY	421	LYRNLSGPDKRLVTLRLPASLAETVTLRPNATYSCVMPDLPGRVPEGEACGEAHT	480
Db	421	LYRNLSGPDKRLVTLRLPASLAETVTLRPNATYSCVMPDLPGRVPEGEACGEAHT	480
QY	481	PPAVSHNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAAQDKGV	540
Db	481	PPAVSHNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRMAAAAQDKGV	540
QY	541	GPGAGPLEGKVKVPLEPGPKATGSGGGEALPGSGECEVPLMGFPFGLOSLPHAKPYI	598
Db	541	GPGAGPLEGKVKVPLEPGPKATGSGGGEALPGSGECEVPLMGFPFGLOSLPHAKPYI	598
RESULT 2			
Q6UXL4 HUMAN			
ID	Q6UXL4	HUMAN PRELIMINARY;	PRT; 673 AA.
AC	Q6UXL4		
DT	05-JUL-2004	(TREMBLrel. 27, Created)	
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)	
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)	
DE	CSRV314	(Slit-like 2).	
GN	Name=SLITL2; ORFNames=UNQ314;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
NCBI_TaxID=9606;			
[1]			
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=22987296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Kilmowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R.L., Watanabe C., Wiscand D., Woods K., Xie M.-H.,		
RA	Yanura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang X., Goddard A.D.,		
RT	Wood W.I., Godowski P.J., Gray A.M.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment."		
RL	Genome Res. 13:2265-2270(2003).		
[2]			
RP	NUCLEOTIDE SEQUENCE		

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Db 181 LLALFPGILDTANVEALRLAGLGLQQLDEGLFSRLRNHLHDLDVSDNQLRVPVIRGLRG 240
Qy 166 LTRLRAGNTRIQAQLRPEDLAGLALQELDVSNLSLQALPGDLGSLFRLRLAAARNPF 225
Db 241 LTRLRAGNTRIQAQLRPEDLAGLALQELDVSNLSLQALPGDLGSLFRLRLAAARNPF 300
Qy 226 NCVPLSWFGPWVRESHVTLASPESTRCHFPKPNAGRLRLLELDYADFCGCPATTTATVPT 285
Db 301 NCVPLSWFGPWVRESHVTLASPESTRCHFPKPNAGRLRLLELDYADFCGCPATTTATVPT 360
Qy 286 TRPVVREPTALSSSLAPTWSLPTAPATAPSPSTAPPTVGPQPCDPCSTCLNGGTC 345
Db 361 TRPVVREPTALSSSLAPTWSLPTAPATAPSPSTAPPTVGPQPCDPCSTCLNGGTC 420
Qy 346 HLGRTRHHLACLCPGEGFTGLYCESQMGQGTSPSTPPTPRPSLTGLIEPVSPSLRVGL 405
Db 421 HLGRTRHHLACLCPGEGFTGLYCESQMGQGTSPSTPPTPRPSLTGLIEPVSPSLRVGL 480
Qy 406 QRYLQSSVOLRSRLTYRNLSGDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGP 465
Db 481 QRYLQSSVOLRSRLTYRNLSGDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGP 540
Qy 466 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 525
Db 541 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 600
Qy 526 RGRAMAAADKQGVGAGGLEGVKVPLEPGPKATEGGGEALPGSGECEVPLMGFP 585
Db 601 RGRAMAAADKQGVGAGGLEGVKVPLEPGPKATEGGGEALPGSGECEVPLMGFP 660
Qy 586 PGLQSPHLHAKPYI 598
Db 661 PGLQSPHLHAKPYI 673

RESULT 3
Q6EMK4_HUMAN
ID Q6EMK4_HUMAN PRELIMINARY; PRT; 673 AA.
AC Q6EMK4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Vasinin.
GN Name=SLITL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15247411; DOI=10.1073/pnas.0404117101;
RA Ikeda Y., Imai Y., Kumagai H., Nosaka T., Morikawa Y., Hisaoka T.,
RA Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,
RA Nagai R., Kitamura T.;
RT "Vasorin, a transforming growth factor (beta)-binding protein
RT expressed in vascular smooth muscle cells, modulates the arterial
RT response to injury in vivo.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).
DR EMBL; AY166584; AA027704.1; -; mRNA.
DR Ensembl; ENSG00000168140; Homo sapiens.
DR HGNC; HGNC:18517; SLITL2.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Cyp.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
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DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR_1; 6.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF_1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00365; LRR_SD22; 4.
DR SMART; SM00369; LRR_TVP; 8.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00853; FN3; 1.
SQ SEQUENCE 673 AA; 71712 MW; 891E149652DEA286 CRC64;

Query Match 98.2%; Score 3078.5; DB 2; Length 673;
Best Local Similarity 88.6%; Pred. No. 2e-165;
Matches 596; Conservative 0; Mismatches 2; Indels 75; Gaps 1;

Qy 1 MCSRVPLLLPLLLLLALPGVQGCPCSCQSQPQTFCTARQGTTPRDPVPPDTVGLYVF 60
Db 1 MCSRVPLLLPLLLLLALPGVQGCPCSCQSQPQTFCTARQGTTPRDPVPPDTVGLYVF 60
Qy 61 ENGITMLDASSFAGLPGQLLDLSQNIAS----- 90
Db 61 ENGITMLDAGSFAGLPGQLLDLSQNIASLPSVGFQPLANLSNLDLTANRLHEITNETF 120
Qy 91 -----LRLPRLLLDLSHNS 105
Db 121 RGLRRLRLYGLKNNRIHQFGAPDTLDRLLELKLQNELRALPPLRPLRLLLDLSHNS 180
Qy 106 LLALFPGILDTANVEALRLAGLGLQQLDEGLFSRLRNHLHDLDVSDNQLRVPVIRGLRG 165
Db 181 LLALFPGILDTANVEALRLAGLGLQQLDEGLFSRLRNHLHDLDVSDNQLRVPVIRGLRG 240
Qy 166 LTRLRAGNTRIQAQLRPEDLAGLALQELDVSNLSLQALPGDLGSLFRLRLAAARNPF 225
Db 241 LTRLRAGNTRIQAQLRPEDLAGLALQELDVSNLSLQALPGDLGSLFRLRLAAARNPF 300
Qy 226 NCVPLSWFGPWVRESHVTLASPESTRCHFPKPNAGRLRLLELDYADFCGCPATTTATVPT 285
Db 301 NCVPLSWFGPWVRESHVTLASPESTRCHFPKPNAGRLRLLELDYADFCGCPATTTATVPT 360
Qy 286 TRPVVREPTALSSSLAPTWSLPTAPATAPSPSTAPPTVGPVPPQPCDPCSTCLNGGTC 345
Db 361 TRPVVREPTALSSSLAPTWSLPTAPATAPSPSTAPPTVGPVPPQPCDPCSTCLNGGTC 420
Qy 346 HLGRTRHHLACLCPGEGFTGLYCESQMGQGTSPSTPPTPRPSLTGLIEPVSPSLRVGL 405
Db 421 HLGRTRHHLACLCPGEGFTGLYCESQMGQGTSPSTPPTPRPSLTGLIEPVSPSLRVGL 480
Qy 406 QRYLQSSVOLRSRLTYRNLSGDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGP 465
Db 481 QRYLQSSVOLRSRLTYRNLSGDKRLVTLRLPASLAEYTVTLRPNATYSVCVMPGLGP 540
Qy 466 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 525
Db 541 GRVPEGEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAAVGAAYCVR 600
Qy 526 RGRAMAAADKQGVGAGGLEGVKVPLEPGPKATEGGGEALPGSGECEVPLMGFP 585
Db 601 RGRAMAAADKQGVGAGGLEGVKVPLEPGPKATEGGGEALPGSGECEVPLMGFP 660
Qy 586 PGLQSPHLHAKPYI 598
Db 661 PGLQSPHLHAKPYI 673

RESULT 4
Q96CX1_HUMAN
ID Q96CX1_HUMAN PRELIMINARY; PRT; 601 AA.
AC Q96CX1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
```

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SLITL2 protein (Fragment).
GN Name=SLITL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC013767; AAH13767.1; -; mRNA.
DR HSSP; Q9BZR6; 1P8T.
DR Ensembl; ENSG00000168140; Homo sapiens.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003591; LRR typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF00560; LRR_1; 6.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR typ; 2.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50853; FN3; 1.
KW EGF-like domain; Leucine-rich repeat.
FT NON_TER 1
SQ SEQUENCE 601 AA; 64178 MW; 4964077F778D9ABD2 CRC64;
Query Match 86.0%; Score 2697.5; DB 2; Length 601;
Best Local Similarity 87.4%; Pred. No. 5.4e-144;
Matches 525; Conservative 0; Mismatches 1; Indels 75; Gaps 1;
Qy 73 AGLFGLQLDLDSQNIAS----- 90
Db 1 AGLFGLQLDLDSQNIASPSGVPFLANLSNLDLTANRLHETITNETFRGLRRLRLYLIG 60

Qy 91 -----LRLPRLLLLDLSHNSLLALEPGLDITA 117
Db 61 KNIRHIQPGAFDTLDRLLLEKLQDNELRALPPURLPRLLLLDLSHNSLLALEPGLDITA 120
Qy 118 NVEALRLAGLGLQQLDRGLFSRLRNLDLVDSDNQLERVPVIRGLRGLRRLRAGNTRI 177
Db 121 NVEALRLAGLGLQQLDRGLFSRLRNLDLVDSDNQLERVPVIRGLRGLRRLRAGNTRI 180
Qy 178 AQLRPEDLAGLAALQELDVSNLSLQALPGDLISGLFPRRLRLAAARNPFCVPLSWFGPW 237
Db 181 AQLRPEDLAGLAALQELDVSNLSLQALPGDLISGLFPRRLRLAAARNPFCVPLSWFGPW 240
Qy 238 VRESHVTLASPEETRCCHFPKKNAGRLLELDYADFGCPATTTTATVTPTRPVVREPTALS 297
Db 241 VRESHVTLASPEETRCCHFPKKNAGRLLELDYADFGCPATTTTATVTPTRPVVREPTALS 300
Qy 298 SSLAPTWLSPTADATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCHLGTRHRLACL 357
Db 301 SSLAPTWLSPTADATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCHLGTRHRLACL 360
Qy 358 PEGFTGLYCSQMGQGRTRPSTPTVTPRPSRLTLGIEPVSPTSRLVGLORYLQSSVOLR 417
Db 361 PEGFTGLYCSQMGQGRTRPSTPTVTPRPSRLTLGIEPVSPTSRLVGLORYLQSSVOLR 420
Qy 418 SLRLTYNLSGPKRLVTLRLPASLAETVTLRPNATYSVCVMPPLGPRVPEGEACGE 477
Db 421 SLRLTYNLSGPKRLVTLRLPASLAETVTLRPNATYSVCVMPPLGPRVPEGEACGE 480
Qy 478 AHTPPAVHSHNAPVTQAREGNLPLLIAPALAAVLLAAVGAAYCVRGRGMAAAADQK 537
Db 481 AHTPPAVHSHNAPVTQAREGNLPLLIAPALAAVLLAAVGAAYCVRGRGMAAAADQK 540
Qy 538 GQVPGGAGPLEEGVKVPLEPGPKATGGGEALPSGSECEVPLMGFPGLQSPHAKPY 597
Db 541 GQVPGGAGPLEEGVKVPLEPGPKATGGGEALPSGSECEVPLMGFPGLQSPHAKPY 600
Qy 598 I 598
Db 601 I 601
RESULT 5
Q8BJU0_MOUSE
ID Q8BJU0_MOUSE PRELIMINARY; PRT; 673 AA.
AC Q8BJU0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:D03006D07 product:hypothetical Prokaryotic membrane
DE lipoprotein lipid attachment site/Cysteine-rich flanking region, N-
DE terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich repeat,
DE typical subtype/Leucine-rich repeat, outliners/Cysteine-rich flanking
DE region, C-terminal/Leucine-rich region/Fibronectin type III domain
DE containing protein, full insert sequence.
GN Name=Slitc12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN 2
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,


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RESULT 6
Q8R2G5_MOUSE PRELIMINARY; PRT; 673 AA.
ID Q8R2G5_MOUSE
AC Q8R2G5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2005 (TrEMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Slit-like 2 protein precursor.
GN Name=Slit2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Muridae;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Schrewe H., Kutejova E.;
RT "Structure and expression analysis of the mouse Slit-like 2 (Slit2)
RT gene.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
EX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458938; CAD30331.1; -; mRNA.
DR EMBL; BC050274; AAH50274.1; -; mRNA.
DR HSSP; P00740; 1EDM.
DR Ensembl; ENSMUSG0000039646; Mus musculus.
DR MGI; MGI:217651; Slit2.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF00560; LRR_1; 6.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_TYP; 3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00853; FN3; 1.
KW Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 673 Slit-like 2 protein.
SQ SEQUENCE 673 AA; 72260 MW; AAB8DA82DA8E9D32 CRC64;

Query Match 79.4%; Score 2490; DB 2; Length 673;
Best Local Similarity 73.5%; Pred. No. 3e-132;
Matches 491; Conservative 25; Mismatches 74; Indels 78; Gaps 3;

QY 6 PLLPLLLLALGFGVQCPSGCSCSQPQTVCFTARQGTTPRDPVPPDVTGLYFENGIT 65
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 PLL--LLLLVLLGSGVQCPSGCSCQCNQPTVCTARQGTTPRDPVPPDVTGLYFENGIT 66
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 66 MLDASSFAGLPGLQLLDLSQNQIAS----- 90
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 TLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLNSLDTANKLHEISNETFRGLRR 126
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 91 -----LRLPRLLLDLSHNSLLALE 110
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 LERLYLGNRIRHIOGAFDALDRLLELKLDPNLRVLPPLHLPRLLLDLSHNSIPALE 186
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 111 PGILDANVEALRLAGLGLQQLDEGLFSRLNLHDLVDNQLRVPVIRGLRGLRLR 170
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 187 AGILDANVEALRLAGLGLRQLDEGLFGRLLNLHDLVDNQLRHPVIRGLRGLRLR 246
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 171 LAGNTRIAQLRPEDLAGLAQLQELVDNLSLQALPGDSLGLFPRLLRLAAARNPFCVCP 230
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 247 LAGNTRIAQLRPEDLAGLTAQLQELVDNLSLQALPSLSSLPRLRLAAARNPFCVCP 306
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 231 LSWFGPWVRESHVTLASPEETRCHFPKNAKRLLELDYADFGCPATTTTATVPTTPV 290
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 LSWFGPWVREHVVLASPEETRCHFPKNAKRLLELDYADFGCPVTTTATVPTTIRTI 366
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 291 REPTALSSSLAPTWSLTAPATEAPSPSTAPPTVGPVQDCCPPSTCLNGTCHLQTR 350
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 367 REPTLSSSQAPTWSLTAPTEPTTQASTVLSTAPPTMRPAQPDQCPASICLNGGSCRLGAR 426
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 351 HHLACLCPGEGTGLYCSCQMGQTRPPTPTVPPRPSLTGLIEPVSPTSRLVGLQRYLQ 410
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 427 HWECCLCPGEGTGLYCSPVEQGMKPSIPTPTPPPLPLSLIEPVSPTSRLVGLQRYLQ 486
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 411 GSSVQLRSRLTYRNLSGPKRLVTLRLPASLAETVTLQLRPNATYSVCMPLGPRVPE 470
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 487 GNTVQLRSRLTYRNLSGPKRLVTLRLPASLAETVTLQLRPNATYSVCMPLGPRVPE 546
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 471 GEEACGEAHTPPAVHSNHPVQTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRRGRAM 530
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 547 GEEACGEANTSQAVRSNHPVQTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRA- 605
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 531 AAAAQDGQVGPAGPLLEGVKVPLBPGPKATGGGEGALPSGSECEVPLMGFPGLQGS 590
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 606 TSTAQDGQVGPAGTGLLEGVKVPLBPGPKATGGGEGALSGPECEVPLMGFPGLQGS 665
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 591 PLHAKPYI 598
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 666 VLPKHYI 673

RESULT 7
Q9CZT5_MOUSE PRELIMINARY; PRT; 673 AA.
ID Q9CZT5_MOUSE
AC Q9CZT5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610528G05 product:hypothetical Prokaryotic
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membrane lipoprotein lipid attachment site/Cysteine-rich flanking region, N-terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich repeat, typical subtype/Leucine-rich repeat, outliers/Cysteine-rich flanking region, C-terminal/Leucine-rich region/Fibronectin type III domain containing protein, full insert sequence.

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning."
Meth. Enzymol. 303:19-44(1999).

[2]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection."
Nature 409:685-690(2001).

[3]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Whole body;
THE FANTOM Consortium.
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
Nature 420:563-573(2002).

[4]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."
Genome Res. 10:1617-1630(2000).

[5]

NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuo S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."
Genome Res. 10:1757-1771(2000).

RNA

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QY 291 REPTALSSSLAPTWSLPTAPATEAPSPSTAPTPVGPVPODQCPSPCLNGTCHLGR 350
Db 367 REPTLSTSSQAPTWPSPLEPTTQASTVLSTAPTPMRPAPQDQCPASCLNGSGSCLGAR 426
QY 351 HHLACLCEPGTGLYCSEMGQGRPSPTPTVTPRPPRLTIGIBPVSPTSRLVGLQRYLQ 410
Db 427 HHWECLCEPGTGLYCSEFVQGMKPSIPDTPRPPPLPLSIFVSPSTSLRVKLQRYLQ 486
QY 411 GSSVOLRLTYRNLSGPDKRLVTLRLPASLAETVTLQRPNTATYSCVNPPLGFRVPE 470
Db 487 GNTVQLRLTYRNLSGPDKRLVTLRLPASLAETVTLQRPNTATYSCVNPPLGFRVPE 546
QY 471 GEEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVRRA- 530
Db 547 GEEACGEAHTPPAVHSHNAPVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVRRA- 605
QY 531 AAAAQDKQVQPGAGPLEGVKVPLEPGPKATEGGGALPSGSECEVPLMGFPGLQGS 590
Db 606 TSTAQDKQVQPGTGLPGLGVKAPLEPGSKATEGGGALSGGPECEVPLMGFPGLQGS 665
QY 591 PLHAKPYI 598
Db 666 VLPKHYI 673

RESULT 8
Q6DF55_XENTR PRELIMINARY; PRT; 661 AA.
AC Q6DF55;
DT 25-OCT-2004 (TREMELrel. 28, Created)
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMELrel. 28, Last annotation update)
DE MGC88956 protein.
GN Name=MGC88956;
OS Xenopus tropicalis (western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RC TISSUE=whole body;
RC TISSUE=whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC076888; AAH76888.1; -; mRNA.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001611; LRR.
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DR InterPro; IPR000483; LRR Cterm.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF01463; LRRCT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00365; LRR_SD22; 4.
DR SMART; SM00369; LRR_TYP; 6.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
SQ SEQUENCE 661 AA; 71957 MW; A0AC47946BE8DBEA CRC64;

Query Match 38.7%; Score 1213.5; DB 2; Length 661;
Best Local Similarity 41.3%; Pred. No. 2.6e-60;
Matches 282; Conservative 88; Mismatches 158; Indels 155; Gaps 20;

QY 8 LLPLLLLLALGPGV--QGCPSGCOCOSOPQVCTAROGTTVPDVPPDTVGLYFENGIT 65
Db 4 LLVWIIILLATAQQMITEGCPAGCQCNTPTQVFCILARKNSNPPRSVPPDTLNLVYFENGIS 63

QY 66 MLDASSPAGLPGLOLLDLSONQIASL----- 91
Db 64 SIESSFIGLNGHLHLLDLSHNLQSSLPGGVFRNLANLSNLDLTNSQLTETISADTFQGLSR 123

QY 92 -----RLPRLLLDLSHNSLLALE 110
Db 124 LERLYLNGNRIRSTHPEAFKGIESLLELKLNNQVTPPAFSLPHLLLLDLSYNAIPVIQ 183

QY 111 PGILDTANVEALRLAGLQLODLGELFSRLNHLHDVSNQDLSEVPVIRGLRGLRLR 170
Db 184 QGVFNAGNIESRLAGLKEVPBELLSGLKNLHDLSDNQLDKVPP--GLHGLTKLN 240

QY 171 LAGNTRIAQLRPEDLAGLAQLDLSNLSIQAIPGDLISGLFRLRLLAARNPNCVCP 230
Db 241 IAGNVGFSQIQVDDLSLALQELDLISGLSLQTLIPKGLFRSSKRLRAVSLAQNPFNCVCS 300

QY 231 LSWFGPVWVRESHVTLAGPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPTTRPVV 290
Db 301 LGWLSEWVRVSGVLLRPDETRCHFPKPNAGKTLRLQRLDSEYGCFA-PTTIQMSTWPP- 358

QY 291 REPTALSSSLAPTWSLPTAP---ATEAPSPSTAPTPVGPVPODQ-----CP 335
Db 359 -----STTTGP-----PTTKHLQTEAPTASTTTTTTIPHQOEEDTQPFQDFEDTLCP 408

QY 336 PSTCLNGTCHLGRHHLACLCPGFTGLYCSEMGQGRPSPTVTPRPPRSL--TLG 392
Db 409 PQTCLNGSGSCHLDPTGQLECCPPGFGQTCYCT-----GPVTPAVVTMIEQVK 458

QY 393 IEPVSPTSRLVGLQRYLQSSVOLRLTYRNLSGPDKRLVTLRLPASLAETVTLQRP 452
Db 459 IIEVTSSIRVDLSQYSQNK-ELRAIRLTVRLNYGADRRPMIYKLPPTLPEYTVRALSS 517

QY 453 NATYSVCVMPILGPRVPEGEACGEAHT---PPAVHSHNAP-VTQAREGNLPLLIAPALA 508
Db 518 NSSYVWCLGSGEGG-PE-EDLCTETHTLGEFP-----KHSQVTSQSGENLTLVLVPAVA 571

QY 509 AVLLAALAAVCAACVRRGRAMAAAAQDKGVGPGAGPLEGVKVPLEPGPKATEGGGE 568
Db 572 AGILLIS-AAVAAAACYARR-----KKGHSVEDGGGLEMDGVK-----KGLDGKE 617

QY 569 AL-----PSGSECEVPLM 581
Db 618 VKLSEDPGTPGPKTGAEESEPLM 640

RESULT 9
Q503G2_BRARE
ID Q503G2_BRARE PRELIMINARY; PRT; 643 AA.
AC Q503G2;
```



```
QY 232 EPTALSSSLAPLWLSPTAPATEAPSPSTAP-----PTVGPVPQPD----- 333
Db 619 SPTGSTPSIPVSTTPPKMTYNAIPPPPPPPSEETLPSKTPVLPPEPTFPSPSTSGEVE 678
QY 334 ---CPPSPSTGGTCHLGRTHHLACLCPGEGFTGLYCESQMGQTRPSPTVTPRPPR--- 387
Db 679 SHICPANICLNGGTCHFDPMGOLSCICLSGTSGLYCEN-----VDIVDPDPKHPV 728
QY 388 ---SUTLGIETP-----VPSLRLVGLQRYLGSSVQLRSRLRYRNLSPGDKRLV 434
Db 729 TEATLAASSVPVQNDAISSRQVTSIILLDLQRFTE-TRPHIRGIRLYRNLSPGDRRPM 787
QY 435 TLRLPASLAETVTLQLRNATYSVCVMDLGP-----GRYPEGEAEAGHT----- 480
Db 788 ILSVPASYPEVTLRGLKKNCTYSVCASPLGRVSRANSSVDTG--SCTEARTGILMNTS 845
QY 481 PPAVHNSHAPVTQAREGNLPLLIAPALAAVLAALAAVGAAYCVRRGRMAAAADQKQV 540
Db 846 SSATAPTPGPMT-----FTLLILAVSALALVGLVSLVAGTVCVRK-RREKAGMELEWA 898
QY 541 GFGAGPLBLEGVKVPLEPGPKATEGGGEALPSG-----SECEVPL 580
Db 899 PADSDPMBLDGKMLGLENANGT-----LPHKQAQINRCHTPL 936
```

RESULT 11

```
Q50LG9_HUMAN
ID Q50LG9_HUMAN PRELIMINARY; PRT; 513 AA.
AC Q50LG9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE LRRC24 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Brain;
RT "Novel gene containing leucine rich repeat on human chromosome 8.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB178281; BAD97811.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR004483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR_1; 5.
DR Pfam; PF01463; LRRCT; 1.
DR PRINTS; PRO00019; LEURICHRPT.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00369; LRR_Typ; 6.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Leucine-rich repeat; Repeat.
SQ SEQUENCE 513 AA; 55199 MW; 3770FA80D979C1DE CRC64;
```

Query Match 11.8%; Score 368.5; DB 2; Length 513;
Best Local Similarity 26.4%; Pred. No. 8.5e-13;
Matches 170; Conservative 63; Mismatches 217; Indels 195; Gaps 28;

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QY 1 MCSRVPLLLPLLLLALGPGVCGSCQSQPQVFCTARQGTTPRDPVDPDTVGLYVF 60
Db 1 MALRAPALLPLLLL-LPLRAAGCPAACRC-YSATVECGALRLRVPLGIPGTQTLFLQ 58
```

```
QY 61 ENGITMLDASSFAGLPGIQLLDLSNQIASLRL-----PRLLLDLSHNSLLALEPG-I 113
Db 59 DNNIARLEPGALAPLAALRRULYHNNSLRALAEAGFAQAPRLLELALTSNLRGURSGAF 118
QY 114 LDTANVEALRLAGLQQLDEGLFSRLRNHLHDVSDNQLERVPPVINGRLGLTRLRLAG 173
Db 119 VGLAQRLVLYLAGNQLARLLDFTFLHLPRLQELHQSIE----- 159
QY 174 NRTIAQLRPEDLAGLALQELDVNSLSQALPGDLSGLFPRLRLLAARNPFCVCPISW 233
Db 160 -----LLEDQALAGLSSLLALDLSRNQLGTTISREALQPLASQLVRLTENPWRCDLHW 214
QY 234 FGPVVRSHVTLASPEETR--CHEPPKNAGLLELLELDYADFGCPATTTTATVPTTRPVR 291
Db 215 LGAWIKEGGQRLTLRDKKIMCAEPPLALQSLLDVSHSLIC-----IPPSVHV-- 264
QY 292 EPTALSSSLAPLWLSPTAPATEAPSPSTAPPTVGPVPQDCPP--STCLNGGTCHLGT 349
Db 265 QPLELTANLGED-LRVACQASGYQP---LVTWRKVPQPREGRPRAQAQLEGGL--LGL 317
QY 350 RHLACLCPGEGF-----TGLY-CESOMGQG-----TRPSP-TPVTPRP 385
Db 318 GHSASDTGSGMLFSLNITLHAAGKYCEASNAGGAARVPPRLLVNASRQPOQPAQPPP 377
QY 386 PRSLTLGIEPVSTSLRVGLQRYLGSSVQLRSRLTYRNLSPGDKRLVTLRLPASLAEY 445
Db 378 PAARPAGSEP----- 387
QY 446 TVTQLRPNATYSVCVMDPLGPRVPEGEACGEAHTPPAVHNSHAPVTQAREGNLPLLIAP 505
Db 388 -----RPEAG-SMAFRALG-----VATQT-----ATAA 409
QY 506 ALAAVLLAALAAVGAAYCVRRGRMAAAADQKQVGPQA-----GP-----LELEGVK- 553
Db 410 AIALALATALLV-AMICRRRRRKKK-----RGPPGEGALFVNDYLDGPFCTFAQLELRD 464
QY 554 -----VPLEPGPKATEGGGEALPSGSECEVPLMGFPFGGLQSP 591
Db 465 ERGHEMFVINSRKLFAEGPAEA---PADCG-PAQG-AGPGLRVP 504
```

RESULT 12

```
LRFN4_HUMAN
ID LRFN4_HUMAN STANDARD; PRT; 635 AA.
AC Q6FUG9; Q9BWJ0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leucine-rich repeat and fibronectin type-III domain containing protein
DE 4 precursor.
GN Name=LRFN4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=Eye, and Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
```

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
 CC
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; BC000207; AAH00207.2; -; mRNA.
 DR EMBL; BC015581; AAH15581.2; -; mRNA.
 DR Ensembl; ENSG00000173621; Homo sapiens.
 DR HGNC; HGNC:28456; LRFN4.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_C2.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_typ.
 DR Pfam; PF00041; fn3; 1.
 DR Pfam; PF00560; LRR_1; 6.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00369; LRR_TYP; 6.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; PS00853; FN3; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat;
 KW Signal; Transmembrane.
 FT SIGNAL 1
 FT CHAIN 17 635
 FT
 FT TOPO_DOM 17 518
 FT TRANSMEM 519 539
 FT TOPO_DOM 540 635
 FT REPEAT 46 70
 FT REPEAT 71 94
 FT REPEAT 95 118
 FT REPEAT 120 142
 FT REPEAT 144 167
 FT REPEAT 168 191
 FT REPEAT 193 216
 FT DOMAIN 281 367
 FT DOMAIN 407 492
 FT CARBOHYD 25 25
 FT CARBOHYD 70 70
 FT CARBOHYD 324 324
 FT CARBOHYD 333 333
 FT CARBOHYD 376 376
 FT CARBOHYD 440 440
 FT DISULFID 302 351
 FT SEQUENCE 635 AA; 66860 MW; 13E66645A17A92EE CRC64;
 Query Match 11.5%; Score 359.5; DB 1; Length 635;
 Best Local Similarity 27.6%; Pred. No. 3.4e-12;
 Matches 169; Conservative 61; Mismatches 281; Indels 101; Gaps 23;
 QY 8 LLPLLALLGPGVQGCPSQCQ---SQPTVFCTARQGTTPRDPDPTVGLVVFENG 64
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 1 MAPPLLALLASGAACPLPCVCNLTSESUSTLCARHGLLFPVPPNDRRTVEURLADNFI 60

QY 65 TMLDASSFAGLPGQLQLDLSONQIASL-----RLPRLLLDLSHSLLALEPGIL-DTA 117
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 61 QALGPPDFRNMGTLDVLTLSRNAITRIGARAFGDLSELSRLSLHLDGNRLVELGTSLRGPV 120
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 118 NVEALRLAGLGLQQLDEGLFSR-LRNHLHDVDSNQLERVP-PVIRGLRGITRLRLAGNT 175
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 121 NLQHLILSGNQLGRIAPGAFDDFLSELDLDSYNNLRQVPWAGIGAMPALHTLNLHDNL 180
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 176 RIAQLRPEDLAGLAALQELDVSNLSLQALPGDLISGLFPLRL-----LLAAARNPFN 226
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 181 -IDALPGAFAQLQSLSLDLTSNRLATLAPD--PLFSRGDAEASAPLVLSFGNPLH 237
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 227 CVCPLSWFGPMWRSHVTLASPEETR-CHPPPPKNAGRLLELDVADYDGCPTATTTATVPT 285
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 238 CANCELMLR-----RLARPDDLETCASPGLAGRYFWAVPGEFSC----- 278
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 286 TRPVVREPTALSSSLATPWLSPATAPAT---EASPPSTAPTPTVGPVPQ-----PQC 336
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 279 -----EPPIARHTQRLWVLEQQRATLRCLALGDPATPMWVGPDRLVGNSSRARAFP 332
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 337 STCLNGGTCHLGRHHLACLIC--PEGFTGLYCE-----SQMGQGRPSPTPTVTPR 384
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 333 NGTLEIGVTGAGDAGGYTCIATNPAGETARVELRLVLALPHGNGSSAEGGPGSDTAAS 392
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 385 PPRSL-----TLGIEP---VPSLRLVQLRYLQSSVQ-LRSLRLTYRNLGGPKRLVTL 436
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 393 ARTAAEGEGTLESEPAVQVTEVTATSLGWSGPGRPADPVMMFQIQYN--SSEDETLIYR 450
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 437 RLPASLAETVTLQRLPNATYSVCMPLGPGRVPEGEA-----CGEHTTPAVHSNAPV 491
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 451 IVPASSHHFLKHLVPGADYDLCLLALSPAAGPSDLTATLLGCAHFSTLPASPLCHALQ 510
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 492 TQAREGNLPLLIAPALAAVLLAALAAVGAAYCYVRRGRAMAAADKQGVGPGAGPLEG 551
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 511 AHVLGGTLTV-----AVCGVLVAALLVFTVALLV-RGRG-----AGNRLPLKLSH 555
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 552 VKVPLEPGPKAT 563
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 QY 556 VQSQTNGGPSPT 567
 Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
 RESULT 13
 LRFN4 MOUSE
 ID LRFN4 MOUSE STANDARD; PRT; 636 AA.
 AC Q80XU8; Q8K3C4;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Leucine-rich repeat and fibronectin type-III domain containing protein
 DE 4 precursor.
 GN Name=Lrfn4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP STRAIN=C57BL/6J; TISSUE=Head;
 RC MSDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Gimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelina A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai K., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaenueishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Havareshizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAINS-FVB/N; TISSUE-Eye, and Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AK081560; BAC38259.1; -; mRNA.
DR EMBL; BC023036; AAH23036.1; -; mRNA.
DR EMBL; BC023156; AAH23156.1; -; mRNA.
DR HSP; Q9BZ86; 1P8T.
DR Ensembl; ENSMUSG00000045045; Mus musculus.
DR MGI; MGI:2385612; Lrrn4.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR_1; 6.
DR PRINTS; PR00019; LEURICHRPT.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 16
FT CHAIN 17 636
FT TOPO_DOM 17 518
FT TRANSMEM 519 539
FT -----
FT Potential.
FT Leucine-rich repeat and fibronectin type-
FT III domain containing protein 4.
FT Extracellular (Potential).
FT Potential.

FT	REPEAT	540	636	Cytoplasmic (Potential).
FT	REPEAT	46	70	LRR 1.
FT	REPEAT	71	94	LRR 2.
FT	REPEAT	95	118	LRR 3.
FT	REPEAT	120	142	LRR 4.
FT	REPEAT	144	167	LRR 5.
FT	REPEAT	168	191	LRR 6.
FT	REPEAT	193	216	LRR 7.
FT	DOMAIN	281	367	Ig-like.
FT	DOMAIN	407	492	Fibronectin type-III.
FT	CARBOHYD	25	25	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	70	70	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	324	324	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	333	333	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	376	376	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	440	440	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	302	351	By similarity.
FT	CONFLICT	503	503	T -> N (in Ref. 2; AAH23156).
FT	SEQUENCE	636 AA;	67252 MW;	1EE86E96CB88BA91 CRC64;

Query Match	11.2%	Score 351;	DB 1;	Length 636;
Best Local Similarity	27.2%	Pred. No. 1e-11;		
Matches 170;	Conservative	62;	Mismatches 276;	Indels 116;
Gaps	25;			

Qy	8	LLPLLILLALPGVQCGPSCQC---	SOPQTVFCTARQGTTPRDVDPDVTGLVFEENGI	64
Db	1	MAPPLLILLASGAACPLPCVCONLSLSTLCNHRGLLFPVNVDRRTVELLADNFI	60	
Qy	65	TMLDASSFAGLPGHLLDLSONQIASI-----RLPRILLDLDSHNSILLAL-EPGILDTA	117	
Db	61	QALGPPDFRNMGLVLTLSRNAITRIGARSFGDLSLSLHLDGNRLVELGSSSLRGPV	120	
Qy	118	NVEALRLAGLQQLDGLFSR-IRNLHLDVSNQLERVP-PVIRGLRGLTRLRAGNT	175	
Db	121	NLOHLILSNQGLRIAPGAFDFLDSLEDLDSVNNLRQVFWAGIGSNPALHTLNLHNL	180	
Qy	176	RIAQRLPDLGLAALQELDVSNLSLQALPGLSLPRLR-----LAAARPFN	226	
Db	181	IDALPGVFAQLSRLDLTNSRLATLADP--PLFSRGDAASPSPLVLSFGNPLH	237	
Qy	227	CVCPLSFWGPMVRESHVTLASPEETR-CHPPPKNAGRLLLLELDYADFGCPATTTATVPT	285	
Db	238	CNCELLMLR-----RLARPDLETSCASPTLAGRYFWAVPEGEFSC-----	278	
Qy	286	TRPVVREPTALSSSLAPTWSPTAPAT---EAPSPSTAPTPTGVPVPOQD-----	333	
Db	279	-----EPPLIARHTQRLWLVEGQATRLCRALGDPVPTMHVG-----PDDLRLVGNSSRA	328	
Qy	334	-CPSTCLNGCTCHLGRHHLALCLC--PEGFTGLYCESQM-----SQGTRPSPTP	380	
Db	329	WAFNGTLEIGVTGAGDAGATYCTATNPAGATARVELRLALPHGGNTSAGGRPGSPD	388	
Qy	381	VTPRPPRSL-----TLGIEP---VSPSTLRVLGRLQYLOQSSVQ-LRSLRLTYRNLSPGDKR	432	
Db	389	IAASARTAAEGEGTLESEPAVQVTEVTATSLVSWGLGRPADPVMFMFQIQYN--SSEDET	446	
Qy	433	LVTURLPASLAETVTLQRLPNATVSVCMPLPGORVPEGEA-----CGEHTTPAVASN	487	
Db	447	LIYRIVPASSHHFLKHLVPGADYDLCLLALSPAAGPSDLTATRLLLGCAHFSTLPATPLC	506	
Qy	488	HAPVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVRRGRMAAAAKDKQGVGPGAPL	547	
Db	507	HALQAHVILGGLTV-----AVGGVILVAALLVFTVALLV-RGRG-----AGNGRLPL	551	
Qy	548	ELEGVKVPLEPGPKATEGGSEALP	571	
Db	552	KLSHVQ-----SQTNGGTSPMP	568	

RESULT 14	Q8BLUO MOUSE
ID	Q8BLUO MOUSE PRELIMINARY;
AC	Q8BLUO; PRT; 660 AA.

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone: A530098L04 product: KIAA0405 (LEUCINE-RICH
DE REPEAT TRANSMEMBRANE PROTEIN FLRT2) homolog (Fibronectin leucine rich
DE transmembrane protein 2)
GN Name=Map4k5; Synonyms=Flrt2;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RC MEDLINE=95279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bernaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Sakazume N., Sano H.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki S., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6xCBA;
RA Haines B.P., Summerbell D., Rigby P.W.J.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy;
RC MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy;
RC NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK041311; BAC30900.1; -; mRNA.
RL EMBL; AY495669; AAR92202.1; -; mRNA.
RL EMBL; BC096471; AAH96471.1; -; mRNA.
RL HSSP; P07359; IM0Z.
RL Ensembl; ENSMUSG0000047414; Mus musculus.
RL MGI; MGI:1925503; Map4k5.
RL GO; GO:0016021; C:integral to membrane; IEA.
RL InterPro; IPR003961; FN III.
RL InterPro; IPR001611; LRR.
RL InterPro; IPR000483; LRR Cterm.
RL InterPro; IPR000372; LRR Nterm.
RL InterPro; IPR003591; LRR typ.
RL InterPro; IPR001211; PhospholipaseA2.
RL Pfam; PF00041; fn3.1.
RL Pfam; PF00560; LRR.1; 8.
RL Pfam; PF01463; LRRCT; 1.
RL Pfam; PF01462; LRRNT; 1.
RL PRINTS; PR00019; LEURICHRPT.


```
DR SMART; SM00060; FN3; 1.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN 1.
KW Leucine-rich repeat; Repeat; Transmembrane.
SQ SEQUENCE 660 AA; 73948 NW; 5C1A9BBA3142C020 CRC64;

Query Match 20.9%; Score 341; DB 2; Length 660;
Best Local Similarity 13.1%; Pred. No. 3.9e-11;
Matches 143; Conservative 85; Mismatches 238; Indels 154; Gaps 19;

QY 4 RVPLLPLLLLLALGPGVQ-----GCPSGCCSQPQVFTCTARQCTTVPRDVPPTVGLY 58
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
11 RGAFILKFWLIIISUGLYLQVSKLLACPSVCRDR-NFYICNERSLTSVPLGIPGEGVTLY 69
QY 59 VP-----ENGINEITMLDASSF 72
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
70 LHNQINNAGPFAELHNQSVHVTYLYGNQLDPEPMNLPKNVRVLHLQENNIQIISRAAL 129
QY 73 AGLPGQLLDLSQNOIASRLP-----RLLLDLDSHNSLLALEPGI---LDTANVEA 121
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
130 AQLLKLEELHLDNISITGVVEDGAFREAIKLLFLSKNHLSSVPVGLPVDLQELRVDE 189
QY 122 LRLA---GLGQLQD-----EGLFSLRLNHLDLVSDNOLERVPEVI 160
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
190 NRIAVISMAFQNTLSRLERLIVDGNLLNKGIAEGTFSHLTKLKEFSIVRNSLSHPDPDL 249
QY 161 RGLRLGLRLRAGNTRIAQLRPEDIAGLAALQELDVSNLSLQALPGDLSGLFPRLRLIAA 220
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
250 PGTH-LRLYLQDN-QINHIPLTAFANLRKLERLDISNNQLRMLTQGVFDHLSNLKQLTA 307
QY 221 ARNPNCVCLSWFGWVRESHTLASPEETRCPPPKNAGRLLELDYADFGCPATTTT 280
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
308 RNNPWFCDSCIKWTEMLKIPSSL-NVRGFMCGPEQVRGMVARELNMLLSCTPTTPG 366
QY 281 ATVPTRPVREPTALSSSLAPTWSLTAPATEAPSPSTAPPTVGPVPQDCPPSTCL 340
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
367 LPVFTFAP-----STVSPTTQPTL-----SVPSRGRGSVFPAPTFPSKLUPTIDW 411
QY 341 NGGTCHLGTRHHLACLCEGFTGLYCSEQMGQGTTPVTPRPRSLTGIGSPVSPTS 400
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
412 DG-----RERVTPPISERIQLSIHFNVDTS 436
QY 401 LRVGLQRYLQSSVOLRLTYRNLSPDKRLVTLRLPASLAEY-TVQLRPNATYSVC 459
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
437 IQVSWLSLFTVMAYKLTVMKGHSIVGG-----IVOERIVSGEKQHLSLVNLEPRSTRIC 492
QY 460 VMPLGGRVPGEAA-CGEATPPA-----VHSNHAPVTQAREGNLPLLIAPALAAVL 511
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
493 LPVLDFAFNRYVEDTICSEATHTASLYLNGSNNTASSHEQTTSNMGWS-PFLLAGLIGAV 551
QY 512 LAALAAVGAAYC---VRRGR 528
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
552 IFVLVLLSVFCWHMKGR 571
PRT; 521 AA.

RESULT 15
Q8BHA1 MOUSE
ID Q8BHA1_MOUSE PRELIMINARY; PRT; 521 AA.
AC Q8BHA1_
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE library, clone:C230002N12 product:hypothetical zinc carboxypeptidases,
DE carboxypeptidase A metalloprotease (M14) family containing protein,
DE full insert sequence (Mus musculus adult male olfactory brain cDNA,
DE RIKEN full-length enriched library, clone:6430402H13
DE product:hypothetical zinc carboxypeptidases, carboxypeptidase A
DE metalloprotease (M14) family containing protein, full insert
DE sequence).
```

GN OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
RX MEDLINE=11217851; PubMed=12185660; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
RX MEDLINE=12466851; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanaai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kogawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RL prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 (5)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama Y., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 (6)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 (7)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 (8)
 DR EMBL; AK048678; BAC33419.1; -; mRNA.
 DR EMBL; AK078176; BAC37163.1; -; mRNA.
 DR HSP; Q9BZR6; 10ZN.
 DR Ensembl; ENSMUSG00000033707; Mus musculus.
 DR MGI; MGI:2445060; Lrrc14.
 DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_cyp.
 DR Pfam; PF00560; LRR_1; 4.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00408; IGG2; 1.
 DR SMART; SM00369; LRR_TYP; 3.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Carboxypeptidase; Hypothetical protein; Immunoglobulin domain;
 KW Leucine-rich repeat; Metalloprotease; Protease; Repeat.
 SQ SEQUENCE 521 AA; 56334 MW; 3D1E4BEE302284A6 CRC64;

Query Match 10.8%; Score 339; DB 2; Length 521;
 Best Local Similarity 27.0%; Pred. No. 4e-11;
 Matches 149; Conservative 66; Mismatches 217; Indels 120; Gaps 21;
 Qy 1 MCSRVPULLPL---LLLLALGPV---OQCPSCQCSPQVFTCTARQGTTPRDPDPPD 53
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 54 TVGLYVPENGITMLDASSFAGLPGQLQLDLSONQIASLR-----LPRLLLDLSHSL 107
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 60 TOTLFQDNSTIAHLEQGS LAPLAARHLYLHNNTLRALES GAFAQAPRLLEALTAUNRLR 119
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 108 ALRPG-ILDTANVEARLGLGLQQLDEGLFSRLNLDLVDSDNQLEVPVIRGLRGL 166
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 120 GLRGAPVGLVQLRVLYLGNLAKLUDFTFLHLPRQLQLHQENSI----- 167
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 167 TRLRLAGNTRIAQLRPEDLAGLAALQBLVDNSLSQALPGDLSGLFRLRLAAARNPFN 226
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 168 -----LLEDQALAGLSLALLDLNRNLGTISKEALQPLSSLOVLRLTENPWR 215
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 227 CVCPLSWFGPVRSHVTLASPETR---CHFPKNAAGRLLELDYADFQCPATTTATVP 284
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 216 CDCALHWLGSWIKEGRRLLSRDKKITCAEPPLRALQSLLEVSGSLIC-----IP 267
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 285 TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQDCPP--STCLNG 342
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 268 PSNVV--EPPEFTANLGED-LQVACQASGVQP-----LVWRKVQPRDGKPOAQALEG 320
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 343 GTCHLG-----TRHHLACLCEPGFTGLY-CESOMQGGTRPSPTPTVTPRPPR 387
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 321 GAPGLGGHGRDGTGSGMLFUTNITLA-----HAGKYECEAANAGGARVPFFHLLVNASR 374
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 388 SLTLGI-EPVSPTSRLVQLQRYLQGSVQLRSRLTYRNLSGPDKRLVTL----- 436
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 375 QSQQLPDPQAPATRPVGHGEPHQEAGSMAPRALGLATQTATTAIALTALLAAMIC 434
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 437 -----RLPASLAEVT-----VTQLRPNATYSVCVM-----PLGPGRVPE 470
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 435 RRRRRKKVPAPSGEGTLFVNDYSDGPTCTPAQLEELDDHGHMFVIDRSKPLFPEVL- 493
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 471 GEEACGEAHTPP 482
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 494 -EEA--PEHNPP 502

Search completed: January 5, 2006, 13:58:27
 Job time : 271 secs

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GenCore version 5.1.6
 OM protein - protein search, using sw model
 Run on: January 5, 2006, 13:52:44 ; Search time 190 Seconds
 (without alignments)
 1382.887 Million cell updates/sec

Title: US-09-943-780-69
 Perfect score: 3135
 Sequence: 1 MCSRVPLLPLLLLLALGPG.....PLMGFPGLQSLHAKPYI 598
 Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
 Total number of hits satisfying chosen parameters: 2443163
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database : A_Geneseq_21.*
 1: Geneseqp1980s.*
 2: Geneseqp1990s.*
 3: Geneseqp2000s.*
 4: Geneseqp2001s.*
 5: Geneseqp2002s.*
 6: Geneseqp2003as.*
 7: Geneseqp2003bs.*
 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AA06484	standard; protein; 598 AA.				
DE	Human tumour-associated protein PRO357.					
PN	W0935170-A2.					
PD	15-JUL-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 2;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 3.8e-190;				
RESULT 2						
ID	AA01322	standard; protein; 598 AA.				
DE	Human PRO357 polypeptide.					
PN	W0200032776-A2.					
PD	08-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 3.8e-190;				
RESULT 3						
ID	AA093691	standard; protein; 598 AA.				
DE	Amino acid sequence of novel polypeptide PRO357.					
PN	W0200037640-A2.					
PD	29-JUN-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 3.8e-190;				
RESULT 4						
ID	AA083643	standard; protein; 598 AA.				
DE	Human PRO protein, Seq ID No 104.					
PN	W0200208288-A2.					
PD	31-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 3.8e-190;				
RESULT 5						
ID	ADY31844	standard; protein; 598 AA.				
DE	Novel human secreted and transmembrane protein PRO357.					
PN	W0200193983-A1.					
PD	13-DEC-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 3135;	DB 5;	Length 598;		
Best Local Similarity	100.0%;	Pred. No. 3.8e-190;				
RESULT 6						
ID	ABU55931	standard; protein; 598 AA.				

DE Human secreted/transmembrane protein PRO357.
 PN US2002142959-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 7
 ID AB080790 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003036635-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 8
 ID ABO33756 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003045687-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 9
 ID AB060241 standard; protein; 598 AA.
 DE Human PRO polypeptide #12.
 PN US2002132768-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 10
 ID AB064927 standard; protein; 598 AA.
 DE Human secreted/transmembrane protein PRO357.
 PN US2002173463-A1.
 PD 21-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 11
 ID AB058361 standard; protein; 598 AA.
 DE Novel human secreted protein PRO357.
 PN US2002150976-A1.
 PD 17-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 12
 ID AB057247 standard; protein; 598 AA.
 DE Human PRO357 protein.
 PN US2002142958-A1.
 PD 03-OCT-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 13
 ID AB056312 standard; protein; 598 AA.
 DE Human secreted/transmembrane protein, PRO357.
 PN US2002132981-A1.
 PD 19-SEP-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 14
 ID AB060352 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2002168715-A1.
 PD 14-NOV-2002.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 3135; DB 6; Length 598;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 RESULT 15
 ID AB082099 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.

PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 16
ID ABU11313 standard; protein; 598 AA.
DE Human pro357 protein sequence.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 17
ID ABU67132 standard; protein; 598 AA.
DE Human PRO polypeptide #12.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 18
ID ABU72279 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 19
ID ABJ72407 standard; protein; 598 AA.
DE Human PRO357 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 20
ID ABO34302 standard; protein; 598 AA.
DE Human secreted/transmembrane polypeptide PRO 357.
PN US2003049334-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 6; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 21
ID ABJ72109 standard; protein; 598 AA.
DE Human membrane bound receptor/protein PRO357 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 22
ID AD883594 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 23
ID AD880700 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US200308068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 24
ID AD873241 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096968-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 25
ID AD878323 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 26
ID AD884971 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 27
ID AD878077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 28
ID AD887143 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US200308067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 29
ID AD884725 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 30
ID AD883840 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 31
ID AD872995 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 32
ID ADC25825 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 33
ID ADC25583 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2002156004-A1.
PD 24-OCT-2002.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 34
ID ADC25704 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003077698-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 35
ID ADC36833 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 36
ID ADC21823 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 37
ID ADC49854 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 38
ID ADC49053 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 39
ID ADC49570 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 40
ID ADC47431 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 41
ID ADC47176 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 42
ID ADC78051 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 43
ID ADD06286 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 44
ID ADC77805 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 45
ID ADD50768 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 46
ID ADD51014 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 47
ID ADD50495 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 48
ID ADD50249 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 49
ID ADD51260 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 50
ID ADH27489 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003083479-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 51
ID ADC48807 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;

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Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 54
ID ADD75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 55
ID ADD75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 56
ID ADD85029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 57
ID ADD86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 58
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 59
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 61
ID ADD73561 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 62
ID ADD78401 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 70
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
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ID ADD85535 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 71
ID ADD805084 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 72
ID ADD75297 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 73
ID ADD76841 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 74
ID ADD86609 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 75
ID ADD78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 76
ID ADE71538 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 77
ID ADD77585 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 78
ID ADD77831 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 79
ID ADD85289 standard; protein; 598 AA.

DE Novel human secreted and transmembrane protein PRO357.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 80
ID ADD73821 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 81
ID ADD74559 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 82
ID ADD77087 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 83
ID ADD85781 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 84
ID ADE05330 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 85
ID ADD74805 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 86
ID ADG05617 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 87
ID ADG2171 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.8e-190;
RESULT 88
ID ADG11234 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.

PN US2003096967-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 89
 ID ADG12013 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096963-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 90
 ID ADF94570 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096964-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 91
 ID ADG06666 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096966-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 92
 ID ADG63481 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003211570-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 93
 ID ADH39010 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096965-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 94
 ID ADH43210 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2003207401-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 95
 ID ADG34100 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2004006206-A1.
 PD 08-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 96
 ID ADI33570 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2003096960-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 97
 ID ADH69664 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2004019183-A1.

PD 29-JAN-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 98
 ID ADI29825 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2003096961-A1.
 PD 22-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 99
 ID ADM27222 standard; protein; 598 AA.
 DE Novel human secreted and transmembrane protein PRO357.
 PN US2004044179-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 100
 ID ADK66580 standard; protein; 598 AA.
 DE Human PRO polypeptide #52.
 PN US2004044180-A1.
 PD 04-MAR-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 101
 ID ADN0448 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2004091972-A1.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 102
 ID ADU25372 standard; protein; 598 AA.
 DE Human secreted/transmembrane PRO polypeptide #12.
 PN US2004220385-A1.
 PD 04-NOV-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
 RESULT 103
 ID ADY39535 standard; protein; 598 AA.
 DE Human insulin-like growth factor homolog PRO357 precursor protein.
 PN US2005048613-A1.
 PD 03-MAR-2005.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 9; Length 598;
 RESULT 104
 ID ADY73816 standard; protein; 598 AA.
 DE Human PRO357 protein, SEQ ID NO: 69.
 PN US2005059115-A1.
 PD 17-MAR-2005.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 100.0%; Score 3135; DB 9; Length 598;
 RESULT 105
 ID AAY17931 standard; protein; 598 AA.
 DE Human PRO357 protein sequence.
 PN WO9928462-A2.
 PD 10-JUN-1999.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 99.7%; Score 3126; DB 2; Length 598;
 RESULT 106
 ID AAB07428 standard; protein; 673 AA.
 DE Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).
 PN WO200042170-A1.
 PD 20-JUL-2000.

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 98.4%; Score 3083.5; DB 3; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 107
ID AAB87533 standard; protein; 673 AA.
DE Human PRO1282.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 108
ID AAB65166 standard; protein; 673 AA.
DE Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 4; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 109
ID AAU75266 standard; protein; 673 AA.
DE Human Slit-like protein #1.
PN WO200212346-A2.
PD 14-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 110
ID ABG95858 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 111
ID ABG78042 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein (LRSG-1).
PN US2002072089-A1.
PD 13-JUN-2002.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MACB/) MACBETH K J.
PA (BUSF/) BUSFIELD S J.
PA (PANY/) PAN Y.
PA (WHIT/) WHITE D.
PA (KHOD/) KHODADOUST M M.
PA (GUW/) GU W.
Query Match 98.4%; Score 3083.5; DB 5; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 112
ID ABU57981 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 113
ID ABU59059 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 114
ID ABU82571 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 115

ID ABU60490 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 116
ID ABU13872 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 117
ID ABU72457 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 118
ID ABU90883 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 119
ID ABO33942 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 120
ID ABU71959 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 121
ID ABU71513 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 122
ID ABU72294 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 123
ID ABU90967 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 124
ID ABU59206 standard; protein; 673 AA.

DE Human secreted/transmembrane protein, #19.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 125
ID ABO25903 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 126
ID ABO27288 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 127
ID ABO2483 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 128
ID ABO81153 standard; protein; 673 AA.
DE Human secreted polypeptide PRO1282.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 129
ID ABO53268 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 130
ID ABO58912 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #19.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 131
ID ABO22290 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 132
ID ABO59355 standard; protein; 673 AA.
DE Novel human secreted or transmembrane protein PRO1282.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 133
ID ABO98270 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 134
ID ABO89275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 135
ID ABO82482 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 136
ID ABO92121 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 137
ID ABO96446 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 138
ID ABO10827 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 139
ID ABO81579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 140
ID ABO72116 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 141
ID ABO88518 standard; protein; 673 AA.
DE Human secreted and transmembrane polypeptide PRO1282.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 142
ID ABO34032 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 143

ID ADB17073 standard; protein; 673 AA.
DE Human transmembrane PRO polypeptide (SeqID 16).
FN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 144
ID ADA37563 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 145
ID ADA21249 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
FN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 146
ID ABO4246 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
FN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 147
ID ADA10036 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, PRO1282.
FN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 148
ID ADA19878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 149
ID ADB17261 standard; protein; 673 AA.
DE Human transmembrane PRO polypeptide (SeqID 16).
FN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 150
ID ADA17580 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
FN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 151
ID ADA27688 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 152
ID ADA20050 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 153
ID ABO34174 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
FN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 154
ID ADA94268 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 155
ID ADA38493 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 156
ID ADA92614 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 157
ID ADA00347 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO 1282.
FN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 6; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 158
ID ABO53118 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 159
ID ADA22175 standard; protein; 673 AA.
DE Human secreted/transmembrane polypeptide PRO1282.
FN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 160
ID ABO22488 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 161
ID ADA06341 standard; protein; 673 AA.
DE Human secreted/transmembrane PRO polypeptide #13.
FN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 162
ID ADA39034 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
FN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 163
ID AD885589 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 164
ID AD896060 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 165
ID AD868268 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 166
ID AD868075 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 167
ID AD890892 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 168
ID ADC57532 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 169
ID ADC54896 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 170
ID ADC11763 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 171
ID ADC06972 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 172
ID ADC56185 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003064375-A1.

PD 03-APR-2003.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 173
ID ADC17151 standard; protein; 673 AA.
DE Mammalian PRO polypeptide (SeqID 16).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 174
ID ADC07240 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 175
ID ADC11230 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 176
ID ADC14849 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 177
ID ADC52344 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 178
ID ADC14352 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 179
ID ADD07884 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 180
ID ADC81709 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 181
ID ADD07351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 182
ID ADC82242 standard; protein; 673 AA.
DE Human PRO polypeptide #13.

PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 183
ID AD08422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 184
ID AD06671 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 185
ID ADC82918 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 186
ID ADD55025 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 187
ID ADD36020 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 188
ID ADD5983 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 189
ID ADD54421 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 190
ID ADE26575 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 191
ID ADE26042 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 192
ID ADF66979 standard; protein; 673 AA.
DE Human PRO1282 amino acid sequence SEQ ID NO:52.

PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 193
ID ADG01021 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 194
ID ADG08574 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 195
ID ADF95195 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 196
ID ADH24048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 197
ID ADH34074 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 198
ID ADH29907 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 199
ID ADH23878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 200
ID ADG85282 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 201
ID ADH24558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180907-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 202
ID ADH37414 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 203
ID ADH02003 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 204
ID ADH37584 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 205
ID ADG85622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 206
ID ADH24218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 207
ID ADH38512 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 208
ID ADG83633 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 209
ID ADH29441 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 210
ID ADH27557 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 211
ID ADH37754 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 212
ID ADH37931 standard; protein; 673 AA.
DE Human secreted and transmembrane protein PRO1282.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 213
ID ADH57351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 214
ID ADH53493 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 215
ID ADH53663 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 216
ID ADH51999 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 217
ID ADH49854 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 218
ID ADI25364 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 219
ID ADH90157 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 220
ID ADI25534 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181659-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 221
ID ADH97708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 222
ID ADH97708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 223
ID ADI35233 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 224
ID ADI03556 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 225
ID ADI11913 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 226
ID ADH89987 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 227
ID ADH99725 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 228
ID ADH98388 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 229
ID ADI11063 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 229

ID ADI11573 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 230
ID ADH98218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 231
ID ADH98558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 232
ID ADH98048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 233
ID ADI05036 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 234
ID ADI03386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 235
ID ADI04781 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 236
ID ADH78235 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 237
ID ADI19579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 238
ID ADH90327 standard; protein; 673 AA.

DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 239
ID ADI03046 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 240
ID ADH77895 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 241
ID ADH97878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 242
ID ADI01263 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 243
ID ADI01958 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 244
ID ADI03216 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 245
ID ADI11403 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 246
ID ADI02305 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 247
ID ADI11743 standard; protein; 673 AA.
DE Human PRO polypeptide #8.

PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 248
ID ADI05380 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 249
ID ADH79452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 250
ID ADI19409 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 251
ID ADI05210 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 252
ID ADH79622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 253
ID ADI01448 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 254
ID ADI01618 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 255
ID ADI01788 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 256
ID ADH79792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191289-A1.

PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 257
ID ADI04610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 258
ID ADI02746 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 259
ID ADH78065 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 260
ID ADI25704 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 261
ID ADI25874 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 262
ID ADK65386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 263
ID ADH98728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 264
ID ADH79969 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 265
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003040013-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 266
ID ADC52154 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 267
ID ADF35178 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
FN US2003194760-A1.
PD 16-OCT-2003.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 268
ID ADG11428 standard; protein; 673 AA.
DE Human PRO1282 polypeptide.
FN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 269
ID ADH06586 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 270
ID ADH06416 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 271
ID ADG68837 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 272
ID ADH27727 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 273
ID ADH25068 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 274
ID ADH33700 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
FN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 275
ID ADL93700 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
FN US2003040013-A1.
PD 27-FEB-2003.

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Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 275
ID ADH02343 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 276
ID ADH07950 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 277
ID ADG69347 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 278
ID ADH39168 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 279
ID ADG83908 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 280
ID ADH19298 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 281
ID ADG85452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 282
ID ADH06246 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 283
ID ADH30076 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 284
ID ADH24388 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 285
ID ADG69517 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 286
ID ADH07780 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 287
ID ADG85792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 288
ID ADH39338 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 289
ID ADH33530 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 290
ID ADH33870 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 291
ID ADH01080 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 292
ID ADG69687 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 293
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ID ADH20791 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 294
ID ADH02173 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 295
ID ADG69177 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 296
ID ADG85962 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 297
ID ADH24898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 298
ID ADH39515 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 299
ID ADH19831 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 300
ID ADH02513 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 301
ID ADG69007 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 302
ID ADH07610 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.

PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 303
ID ADG86132 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 304
ID ADH24728 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 305
ID ADH25776 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 306
ID ADH38342 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 307
ID ADH57181 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 308
ID ADH52169 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 309
ID ADH49535 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 310
ID ADH90497 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 311
ID ADH11233 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181683-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 312
ID ADH98898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 313
ID ADJ02128 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 314
ID ADH98667 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 315
ID ADJ98542 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 316
ID ADJ98712 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 317
ID ADH78871 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 318
ID ADJ99105 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 319
ID ADJ99275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 320
ID ADJ98893 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 321
ID ADH79041 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 322
ID ADK0901 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 323
ID ADK14422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 324
ID ADM80871 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 325
ID ADR45587 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 326
ID ADY77711 standard; protein; 673 AA.
DE Neoplastic disease detection protein PRO1282.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 327
ID AEA38367 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #81.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.1e-187;
RESULT 328
ID AAB84689 standard; protein; 673 AA.
DE Amino acid sequence of human slit polypeptide Zslit3.
PN WO200146418-A1.
PD 28-JUN-2001.
PA (ZYMO) ZYMOGENETICS INC.

Query Match 98.2%; Score 3078.5; DB 4; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.7e-186;
RESULT 329
ID ADF69108 standard; protein; 673 AA.
DE Human MP53 protein sequence SEQ ID NO:78.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 98.2%; Score 3078.5; DB 7; Length 673;
Best Local Similarity 88.6%; Pred. No. 1.7e-186;
RESULT 330
ID AB059449 standard; protein; 676 AA.
DE Human genome derived single exon protein #5683.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 98.2%; Score 3078.5; DB 8; Length 676;
Best Local Similarity 88.6%; Pred. No. 1.7e-186;
RESULT 331
ID ADA57213 standard; protein; 672 AA.
DE Human secreted protein #496.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.1e-177;
RESULT 332
ID ADA41092 standard; protein; 672 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.1e-177;
RESULT 333
ID ABR47923 standard; protein; 672 AA.
DE Human secreted protein, SEQ ID 814.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 6; Length 672;
Best Local Similarity 85.2%; Pred. No. 2.1e-177;
RESULT 334
ID AAB38323 standard; protein; 673 AA.
DE Human secreted protein encoded by gene 3 clone HSAV50.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 3; Length 673;
Best Local Similarity 85.2%; Pred. No. 2.1e-177;
RESULT 335
ID AAB38400 standard; peptide; 723 AA.
DE Fragment of human secreted protein encoded by gene 3 clone HSAV50.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 93.6%; Score 2935; DB 3; Length 723;
Best Local Similarity 85.2%; Pred. No. 2.2e-177;
RESULT 336
ID AAU75267 standard; protein; 630 AA.
DE Human slit-like protein #2.
PN WO200212346-A2.
PD 14-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match 90.8%; Score 2845.5; DB 5; Length 630;
Best Local Similarity 85.2%; Pred. No. 8.9e-172;
RESULT 337
ID AAY66643 standard; protein; 611 AA.
DE Membrane-bound protein PRO1282.
PN WO9963088-A2.
PD 09-DEC-1999.

PA (GETH) GENENTECH INC.
Query Match 86.5%; Score 2712.5; DB 3; Length 611;
Best Local Similarity 79.5%; Pred. No. 2.3e-163;
RESULT 338
ID ABG78046 standard; protein; 673 AA.
DE Mouse leucine-rich surface glycoprotein (LRSG-1).
PN US2002072089-A1.
PD 13-JUN-2002.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (MACB/) MACBETH K J.
PA (BUSF/) BUSFIELD S J.
PA (PANY/) PAN Y.
PA (WHIT/) WHITE D.
PA (KHOD/) KHODADOUST M M.
PA (GUWW/) GU W.
Query Match 79.4%; Score 2490; DB 5; Length 673;
Best Local Similarity 73.5%; Pred. No. 3.2e-149;
RESULT 339
ID ADR45596 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #2.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 79.4%; Score 2490; DB 8; Length 673;
Best Local Similarity 73.5%; Pred. No. 3.2e-149;
RESULT 340
ID ADA00753 standard; protein; 673 AA.
DE Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.
PN WO2003018805-A1.
PD 06-MAR-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (NINA-) JAPAN NAT CANCER CENT.
Query Match 79.2%; Score 2484; DB 6; Length 673;
Best Local Similarity 73.4%; Pred. No. 7.7e-149;
RESULT 341
ID AAB07431 standard; protein; 493 AA.
DE A leucine-rich surface glycoprotein (LRSG).
PN WO200042170-A1.
PD 20-JUL-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 53.3%; Score 1672; DB 3; Length 493;
Best Local Similarity 53.3%; Pred. No. 1.5e-97;
RESULT 342
ID ABB72324 standard; protein; 281 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 648.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 37.6%; Score 1178.5; DB 5; Length 281;
Best Local Similarity 80.7%; Pred. No. 1.4e-66;
RESULT 343
ID AAO30403 standard; protein; 311 AA.
DE Human secreted protein (SECP)-6.
PN WO2003046196-A1.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.8%; Score 997.5; DB 7; Length 311;
Best Local Similarity 68.7%; Pred. No. 4.6e-55;
RESULT 344
ID ABR58506 standard; protein; 307 AA.
DE Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.
PN WO2003029437-A2.
PD 10-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 31.3%; Score 980.5; DB 6; Length 307;
Best Local Similarity 67.9%; Pred. No. 5.5e-54;
RESULT 345
ID AAO30821 standard; protein; 117 AA.
DE Human cell adhesion and extracellular matrix protein (CADECM)-11.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 15.0%; Score 471; DB 7; Length 117;
Best Local Similarity 98.9%; Pred. No. 3.4e-22;
RESULT 346
ID AAE23980 standard; protein; 635 AA.
DE Human LP220 secreted protein.
PN WO200226801-A2.
PD 04-APR-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 11.5%; Score 360.5; DB 5; Length 635;
Best Local Similarity 27.1%; Pred. No. 2.4e-14;
RESULT 347
ID ABP70142 standard; protein; 647 AA.
DE Human NOV44a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.5%; Score 360.5; DB 5; Length 647;
Best Local Similarity 27.1%; Pred. No. 2.5e-14;
RESULT 348
ID AAO26256 standard; protein; 635 AA.
DE MDDR related human protein SEQ ID No 34.
PN WO200296951-A1.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.5%; Score 359.5; DB 6; Length 635;
Best Local Similarity 27.6%; Pred. No. 2.8e-14;
RESULT 349
ID AD0209859 standard; protein; 635 AA.
DE Human breast cancer marker MGC3103 protein.
PN EP1522594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 11.5%; Score 359.5; DB 9; Length 635;
Best Local Similarity 27.6%; Pred. No. 2.8e-14;
RESULT 350
ID ABP70144 standard; protein; 778 AA.
DE Human NOV44c.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 11.4%; Score 357.5; DB 5; Length 778;
Best Local Similarity 26.7%; Pred. No. 4.8e-14;
RESULT 351
ID ADN90979 standard; protein; 545 AA.
DE Human pharmacologically useful protein SeqID 372.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 11.2%; Score 350.5; DB 8; Length 545;
Best Local Similarity 27.9%; Pred. No. 8.7e-14;
RESULT 352
ID ABP70143 standard; protein; 566 AA.
DE Human NOV44b.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.8%; Score 339; DB 5; Length 566;
Best Local Similarity 26.9%; Pred. No. 4.9e-13;
RESULT 353
ID AAB17484 standard; protein; 551 AA.
DE Human leucine-rich repeat-8 (ZLR8) protein #2.
PN WO200202604-A2.
PD 10-JAN-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.8%; Score 338; DB 5; Length 551;
Best Local Similarity 27.4%; Pred. No. 5.5e-13;
RESULT 354
ID AD121104 standard; protein; 618 AA.
DE Novel human protein #79.
PN WO2003025148-A2.
PD 27-MAR-2003.

PA (HYSE-) HYSEQ INC. 10.7%; Score 337; DB 7; Length 618;
Query Match 27.2%; Pred. No. 7.2e-13;
Best Local Similarity 27.2%; Pred. No. 7.2e-13;
RESULT 355
ID ADA23287 standard; protein; 653 AA.
DE Human SECX polypeptide, SEC5 #1.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.7%; Score 337; DB 6; Length 653;
Best Local Similarity 23.6%; Pred. No. 7.7e-13;
RESULT 356
ID AAB23033 standard; protein; 694 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.7%; Score 337; DB 3; Length 694;
Best Local Similarity 23.6%; Pred. No. 8.3e-13;
RESULT 357
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 10.6%; Score 333; DB 3; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.2e-12;
RESULT 358
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match 10.6%; Score 333; DB 6; Length 590;
Best Local Similarity 25.8%; Pred. No. 1.2e-12;
RESULT 359
ID ABG04827 standard; protein; 526 AA.
DE Novel human diagnostic protein #4818.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC. 10.6%; Score 332; DB 4; Length 526;
Query Match 26.9%; Pred. No. 1.2e-12;
Best Local Similarity 26.9%; Pred. No. 1.2e-12;
RESULT 360
ID AAY28806 standard; protein; 653 AA.
DE CC359 4 secreted protein.
PN WO9950405-A1.
PD 07-OCT-1999.
PA (GEMY) GENETICS INST INC.
Query Match 10.5%; Score 330; DB 2; Length 653;
Best Local Similarity 24.2%; Pred. No. 2.1e-12;
RESULT 361
ID AAY66694 standard; protein; 653 AA.
DE Membrane-bound protein PRO1111.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC. 10.5%; Score 330; DB 3; Length 653;
Query Match 24.3%; Pred. No. 2.1e-12;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 362
ID AAB24073 standard; protein; 653 AA.
DE Human PRO1111 protein sequence SEQ ID NO:46.
PN WO200053755-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 3; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 363
ID AAU12390 standard; protein; 653 AA.
DE Human PRO1111 polypeptide sequence.
PN WO200140466-A2.

PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 364
ID ABO29438 standard; protein; 653 AA.
DE Human sbgPRO331a protein.
PN WO200160850-A1.
PD 23-AUG-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 365
ID AAB65217 standard; protein; 653 AA.
DE Human PRO1111 (UNQ0554) protein sequence SEQ ID NO:229.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 4; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 366
ID ABUS8032 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 367
ID ABUS9110 standard; protein; 653 AA.
DE Novel human secreted or transmembrane protein PRO1111.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 368
ID ABUS2622 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 369
ID ABO17834 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 370
ID ABUS0541 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 371
ID ABUS1923 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 372
ID ABUS1088 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 373
ID ABUS72508 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 374
ID ABUS6788 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 375
ID AAO23105 standard; protein; 653 AA.
DE NAG14 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 376
ID ABUS9869 standard; protein; 653 AA.
DE Novel secreted and transmembrane protein PRO1111.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 377
ID ABUS9257 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 378
ID ABO25954 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 379
ID ABO25059 standard; protein; 653 AA.
DE Human secreted/transmembrane protein (PRO) #219.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 380
ID ABUS8963 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #93.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 381
ID ABUS2341 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 382

ID ABU59406 standard; protein; 653 AA.
DE Novel human secreted or transmembrane protein PRO1344.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 383
ID ABU67064 standard; protein; 653 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 438.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 384
ID ABU92172 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 385
ID ABU10878 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 386
ID ABU81630 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 387
ID ABU88569 standard; protein; 653 AA.
DE Human secreted and transmembrane polypeptide PRO1111.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 388
ID ABO34083 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 389
ID ADA45957 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 390
ID ADA76388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003037312-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 391
ID ADA19038 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003054517-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 392
ID ADA61661 standard; protein; 653 AA.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 393
ID ADB19446 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 394
ID ADB27987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 395
ID ADA86466 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 396
ID ADB16030 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 397
ID ADA37740 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 398
ID ADA47816 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 399
ID ADA21426 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 400
ID ADA10213 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, PRO1111.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;

RESULT 401
ID ADA67611 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 402
ID ADB30618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 403
ID ADA85914 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 404
ID ADA17757 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 405
ID ADA97126 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 406
ID ADA79430 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 407
ID ADA87569 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 408
ID ADB16771 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 409
ID ADA27865 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 410
ID ADA91863 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003077113-A1.
PD 24-APR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 411
ID ADB14926 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 412
ID ADB18887 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 413
ID ADA94102 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 414
ID ADB19998 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 415
ID ADB13310 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 416
ID ABO43367 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 417
ID ADA94445 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 418
ID ADA74564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 419
ID ADB24797 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077113-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 420
ID ADB25357 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
FN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 421
ID ADA75284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 422
ID ADA85362 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 423
ID ADA84810 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 424
ID ADB30066 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 425
ID ADA80594 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 426
ID ADA75836 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 427
ID ADA38670 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
FN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 428
ID ADA47061 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 429
ID ADB25357 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
FN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 430
ID ADA93533 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 431
ID ADB26883 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 432
ID ADB31170 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 433
ID ADA92791 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
FN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 434
ID ADA61098 standard; protein; 653 AA.
DE Homo sapiens.
FN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 435
ID ADB24245 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
FN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 436
ID ADA96574 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 437
ID ADA81146 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 438
ID ADA81146 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;

ID ADA96022 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 439
ID ADB26331 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 440
ID ADB21816 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 6; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 441
ID ADA77595 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 442
ID ADB18335 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 443
ID ADA87018 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 444
ID ADA88121 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 445
ID ADA46509 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 446
ID ADB28539 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 447
ID ADB29091 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 448
ID ABO53169 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
FN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 449
ID ADA77043 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 450
ID ADA22352 standard; protein; 653 AA.
DE Human secreted/transmembrane polypeptide PRO1111.
FN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 451
ID ADA86673 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 452
ID ADA97678 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 453
ID ADB27435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 454
ID ADB23268 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 455
ID ABO22539 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
FN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 456
ID ADA06518 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO polypeptide #64.
FN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 457

ID ADA39211 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 458
ID ADA67059 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 459
ID ADB22920 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 460
ID ADB23693 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 461
ID ADA92415 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 462
ID ADB15478 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 463
ID ADB38730 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 464
ID ADB96237 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 465
ID ADB38178 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 466
ID ADB66650 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082689-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 467
ID ADB89730 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 468
ID ADB90462 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 469
ID ADB39563 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 470
ID ADB47186 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 471
ID ADB86793 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 472
ID ADB77398 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 473
ID ADB34555 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 474
ID ADB35659 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 475
ID ADB34003 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077716-A1.
PD 24-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 476
ID ADB35107 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 477
ID ADB36211 standard; protein; 653 AA.
DE Human PRO polypeptide SEQ ID NO 438.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 478
ID ADB46606 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 479
ID ADC57709 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 480
ID ADC55073 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 481
ID ADC11940 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 482
ID ADC56362 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 483
ID ADC07417 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 484
ID ADC11407 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 485
ID ADC50479 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092106-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 486
ID ADC72026 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 487
ID ADC60005 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 488
ID ADC53012 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 489
ID ADC57366 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 490
ID ADC60557 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 491
ID ADC51032 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 492
ID ADC65559 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 493
ID ADC54657 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 494
ID ADC53618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087364-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 495
ID ADC59141 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein seq ID438.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 496
ID ADC56019 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein seq ID438.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 497
ID ADC58589 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein seq ID438.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 498
ID ADC14529 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 499
ID ADD08061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 500
ID ADD03263 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 501
ID ADC90255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 502
ID ADC81886 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 503
ID ADC69674 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 504
ID ADC48563 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 505
ID ADD10092 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 506
ID ADD07528 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 507
ID ADD04667 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 508
ID ADC82419 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 509
ID ADC80623 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 510
ID ADD11130 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 511
ID ADC48011 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 512
ID ADD08599 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 513
ID ADC80071 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087358-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 514
ID ADD06848 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 515
ID ADD09540 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 516
ID ADC83095 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 517
ID ADD41253 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 518
ID ADD52392 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 519
ID ADD53132 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 520
ID ADD53684 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 521
ID ADD55202 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 522
ID ADD56160 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 523
ID ADD51840 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 524
ID ADD02639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 525
ID ADD02073 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 526
ID ADD54255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 527
ID ADD54598 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 528
ID ADD92572 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 529
ID ADD91468 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 530
ID ADE04082 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 531
ID ADE26752 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 532
ID ADE32379 standard; protein; 653 AA.

DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 533
ID ADE22311 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 534
ID ADE79535 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 535
ID ADE42071 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 536
ID ADE17888 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 537
ID ADE92020 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 538
ID ADE33483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 539
ID ADE34035 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 540
ID ADE80087 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 541
ID ADE93124 standard; protein; 653 AA.
DE Human PRO polypeptide #219.

PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 542
ID ADE19544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 543
ID ADE18992 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 544
ID ADE43188 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 545
ID ADE95977 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 546
ID ADE22863 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 547
ID ADE78981 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 548
ID ADE26219 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 549
ID ADE32931 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 550
ID ADE42623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199032-A1.
PD 23-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 551
ID ADG80639 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 552
ID ADG89667 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 553
ID ADB40951 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 554
ID ADS04750 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 555
ID ADS92879 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 556
ID ADF67156 standard; protein; 653 AA.
DE Human PRO1111 amino acid sequence SEQ ID NO:229.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 557
ID ADG21588 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 558
ID ADG32329 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 559
ID ADP97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 560
ID ADG80628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 561
ID ADG80076 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 562
ID ADH53368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 563
ID ADH55920 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 564
ID ADI35410 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 565
ID ADI64139 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 566
ID ADI65088 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 567
ID ADI63987 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 568
ID ADH82001 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 569
ID ADP97564 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

RESULT 569
ID ADH99902 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 570
ID ADH81449 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 571
ID ADH82618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 572
ID ADN16017 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 573
ID ADN1646 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 574
ID ADN15465 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 575
ID ADN14913 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 576
ID ADC81175 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 577
ID ADD76623 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 578
ID ADB87987 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 579
ID ADB86391 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 580
ID ADE75839 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 581
ID ADE23415 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 582
ID ADE23967 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 583
ID ADE24610 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 584
ID ADD87435 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 585
ID ADE89301 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 586
ID ADE18440 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 587
ID ADB88749 standard; protein; 653 AA.
DE Human PRO polypeptide #219.

PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 597
ID ADG11605 standard; protein; 653 AA.
DE Human PRO1111 polypeptide.
FN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 598
ID ADG02354 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 599
ID ADG22140 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 600
ID ADG20210 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 601
ID ADF98116 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 602
ID ADG24333 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 603
ID ADF98687 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 604
ID ADG03518 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 605
ID ADF99239 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 598
ID ADE94769 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 599
ID ADE91180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 591
ID ADE95321 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 592
ID ADE93431 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 593
ID ADF35012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 594
ID ADE92327 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 595
ID ADE90628 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
FN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 596
ID ADE91775 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
FN US2003199058-A1.
PD 23-OCT-2003.

RESULT 624
ID ADG56971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 625
ID ADG55867 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 626
ID ADG58627 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 627
ID ADG70993 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 628
ID ADG58075 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 629
ID ADG51659 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 630
ID ADG71545 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 631
ID ADG81732 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 632
ID ADH19475 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 633
ID ADH30694 standard; protein; 653 AA.

DE Human PRO polypeptide #219.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 634
ID ADH12061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 635
ID ADG52483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 636
ID ADG54211 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 637
ID ADG81180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 638
ID ADG56419 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 639
ID ADH12685 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 640
ID ADH20968 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 641
ID ADG61531 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 642
ID ADH20008 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003219856-A1.

PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 643
ID ADH28618 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 644
ID ADG54763 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 645
ID ADG59803 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 646
ID ADI18127 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 647
ID ADG09970 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 648
ID ADI15441 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 649
ID ADG09318 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 650
ID ADI14773 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 651
ID ADI18368 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 652
ID ADJ3649 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 653
ID ADJ7544 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 654
ID ADJ6566 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 655
ID ADM27802 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 656
ID ADM42526 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 657
ID ADM28388 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 658
ID ADI95870 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 659
ID ADI96422 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 660
ID ADS32374 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 661
ID ADT03358 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 662
ID AD203409 standard; protein; 653 AA.
DE Human secreted/transmembrane PRO1111 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 663
ID AEA38492 standard; protein; 653 AA.
DE Human secreted/transmembrane protein, #132.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 664
ID AEA23332 standard; protein; 653 AA.
DE Tumor antigen of hematopoietic origin TAH015.
PN WO2005049075-A2.
PD 02-JUN-2005.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 665
ID ABE14155 standard; protein; 653 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 438.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.5%; Score 330; DB 9; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.1e-12;
RESULT 666
ID ABU12069 standard; protein; 775 AA.
DE Human NOV15a CG92531-01 protein SEQ ID 58.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.5%; Score 329.5; DB 6; Length 775;
Best Local Similarity 26.0%; Pred. No. 2.8e-12;
RESULT 667
ID ABG98014 standard; protein; 649 AA.
DE Human leucine rich repeat domain protein associated protein #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.5%; Score 329; DB 5; Length 649;

Best Local Similarity 24.6%; Pred. No. 2.5e-12;
RESULT 668
ID ADS98753 standard; protein; 824 AA.
DE Protein factor discovery related human contig polypeptide, SEQ ID 1017.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 10.5%; Score 329; DB 8; Length 824;
Best Local Similarity 25.5%; Pred. No. 3.3e-12;
RESULT 669
ID ABG34079 standard; protein; 627 AA.
DE Human Pro peptide #51.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 5; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 670
ID ADA01368 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 671
ID ADA43797 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 672
ID ADA43565 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 673
ID ADA01240 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 674
ID ADA01124 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 675
ID ADA43681 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 676
ID ADA06943 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;

Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 677
ID ADA08431 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
FN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 678
ID ADB99724 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
FN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 679
ID ADB87007 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
FN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 680
ID ADB66162 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 681
ID ADB99840 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
FN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 682
ID ADB99495 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
FN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 683
ID ADB66046 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 684
ID ADC23444 standard; protein; 627 AA.
DE Human transmembrane PRO polypeptide (SeqID 100).
FN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 685
ID ADC26137 standard; protein; 627 AA.
DE Human PRO34192 protein.
FN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 686
ID ADE04964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
FN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 687
ID ADE11270 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
FN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 688
ID ADB8201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
FN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 689
ID ADB95496 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 690
ID ADE06426 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
FN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 691
ID ADE38201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
FN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 692
ID ADB88317 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
FN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 693
ID ADD90898 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 694
ID ADF99453 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
FN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 695

ID ADG06546 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 696
ID ADG05497 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 697
ID ADG82498 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 698
ID ADG51751 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 699
ID ADE51867 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 700
ID ADE37725 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 701
ID ADE37609 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 702
ID ADP95380 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 703
ID ADE38080 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 704
ID ADE76169 standard; protein; 627 AA.

DE Human PRO polypeptide #50.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 705
ID ADE39492 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 706
ID ADE04296 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 707
ID ADE39893 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 708
ID ADE19758 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 709
ID ADE77336 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 710
ID ADE65444 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 711
ID ADE76053 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 712
ID ADE37964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 713
ID ADE64574 standard; protein; 627 AA.
DE Human PRO polypeptide #50.


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PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 714
ID ADE38909 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 715
ID ADE51983 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 716
ID ADE91014 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 717
ID ADE38793 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 718
ID ADE37493 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 719
ID ADE06309 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 720
ID ADD90169 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 721
ID ADE38677 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 722
ID ADE39608 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 723
ID ADD89213 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 724
ID ADD8980 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 725
ID ADE19874 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 726
ID ADE77452 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 727
ID ADE65328 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 728
ID ADE39376 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 729
ID ADE38561 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 730
ID ADG11114 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 731
ID AFG10998 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003077743-A1.
PD 24-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 732
ID ADH31526 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide #50.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 733
ID ADH38774 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 734
ID ADH29409 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 735
ID ADH23712 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 736
ID ADH27042 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 737
ID ADH38310 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 738
ID ADH26926 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 739
ID ADH38194 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 740
ID ADH38890 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 741
ID ADH23828 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 742
ID ADH40203 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 743
ID ADH40088 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 744
ID ADH31410 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide #50.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 745
ID ADH29288 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 746
ID ADH49503 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 747
ID ADH51967 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 748
ID ADH49822 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 749
ID ADH52423 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 750
ID ADH38990 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 750
ID AAG65805 standard; protein; 628 AA.
DE Human leucine-rich repeat (LRR) family member, 33395 polypeptide.
PN WO200172827-A2.
PD 04-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 324; DB 4; Length 628;
Best Local Similarity 24.1%; Pred. No. 4.9e-12;
RESULT 760
ID ADN95165 standard; protein; 810 AA.
DE Human BEC/LEC-related protein sequence SeqID87.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 810;
Best Local Similarity 22.0%; Pred. No. 8.2e-12;
RESULT 761
ID ABR58642 standard; protein; 811 AA.
DE Human cancer related protein SEQ ID NO:299.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 762
ID AO23114 standard; protein; 811 AA.
DE KTA0644 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.3%; Score 322.5; DB 6; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 763
ID ADN95110 standard; protein; 811 AA.
DE Human LEC protein sequence SeqID32.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 10.3%; Score 322.5; DB 7; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 764
ID AQ21196 standard; protein; 811 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 10.3%; Score 322.5; DB 8; Length 811;
Best Local Similarity 22.0%; Pred. No. 8.3e-12;
RESULT 765
ID ADR45590 standard; protein; 605 AA.
DE Homologue of LRSG-1, baboon ALS.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.3%; Score 322; DB 8; Length 605;
Best Local Similarity 36.2%; Pred. No. 6.3e-12;
RESULT 766
ID AAG67523 standard; protein; 628 AA.
DE Amino acid sequence of a human secreted polypeptide.
PN WO200166690-A2.
PD 13-SEP-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 10.2%; Score 321; DB 4; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 767
ID ABR4469 standard; protein; 628 AA.
DE Amino acid sequence of an interferon omega-1 like protein NOV2.
PN WO200142471-A2.
PD 14-JUN-2001.
PA (CURA-) CURAGEN CORP.

Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 750
ID ADH52539 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 751
ID ADH5836 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 752
ID ADH51851 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 753
ID ADH58412 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 754
ID ADI13609 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 755
ID ADK00865 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 756
ID ADJ08606 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 8; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.5e-12;
RESULT 757
ID AAU32870 standard; protein; 636 AA.
DE Novel human secreted protein #361.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.4%; Score 327.5; DB 4; Length 636;
Best Local Similarity 24.2%; Pred. No. 3e-12;
RESULT 758
ID AB08499 standard; protein; 626 AA.
DE Mouse cancer-associated protein MP14-035.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.3%; Score 324; DB 8; Length 626;
Best Local Similarity 24.3%; Pred. No. 4.9e-12;

Query Match 10.2%; Score 321; DB 4; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 768
ID ABP69326 standard; protein; 628 AA.
DE Human polypeptide SEQ ID NO 1373.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 10.2%; Score 321; DB 5; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 769
ID ADP69107 standard; protein; 628 AA.
DE Human MP53 protein sequence SEQ ID NO:77.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 321; DB 7; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 770
ID ADH71652 standard; protein; 628 AA.
DE Human protein of the invention NOV22a SEQ ID NO:548.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 771
ID ADH71654 standard; protein; 628 AA.
DE Human protein of the invention NOV22b SEQ ID NO:550.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 772
ID AB084502 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.3.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 773
ID AB084503 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.4.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 774
ID AB084501 standard; protein; 628 AA.
DE Human cancer-associated protein HP14-035.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 10.2%; Score 321; DB 8; Length 628;
Best Local Similarity 23.9%; Pred. No. 7.6e-12;
RESULT 775
ID ABP70928 standard; protein; 762 AA.
DE Human LP341 protein.
PN WO2003029778-A2.
PD 10-APR-2003.
PA (ELIL) LILLY & CO ELI.
Query Match 10.2%; Score 321; DB 6; Length 762;
Best Local Similarity 25.5%; Pred. No. 9.6e-12;
RESULT 776
ID ADI36917 standard; protein; 797 AA.
DE Human LRR protein #12.
PN US2003220263-A1.
PD 27-NOV-2003.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.

PA (RAMA/) RAMANATHAN C S.
Query Match 10.2%; Score 321; DB 8; Length 797;
Best Local Similarity 25.5%; Pred. No. 1e-11;
RESULT 777
ID ADS98018 standard; protein; 803 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 282.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
Query Match 10.2%; Score 321; DB 8; Length 803;
Best Local Similarity 25.5%; Pred. No. 1e-11;
RESULT 778
ID AAY13349 standard; protein; 660 AA.
DE Amino acid sequence of protein PRO265.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 2; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 779
ID ADC78348 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 3; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 780
ID AAB80217 standard; protein; 660 AA.
DE Human PRO265 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 781
ID AAB31208 standard; protein; 660 AA.
DE Amino acid sequence of human polypeptide PRO265.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 782
ID AAU12346 standard; protein; 660 AA.
DE Human PRO265 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 4; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 783
ID ABB84839 standard; protein; 660 AA.
DE Human PRO265 protein sequence SEQ ID NO:46.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 784
ID ABB95445 standard; protein; 660 AA.
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 5; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 785
ID ABU71595 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 786
ID AB017790 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 787
ID AB071450 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 788
ID AB025179 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 789
ID ABU81044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 790
ID ABU71896 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 791
ID AB001779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 792
ID ABU66744 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 793
ID ABU54352 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 794
ID ABU67297 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 795
ID AAO23116 standard; protein; 660 AA.
DE FLRT2 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 796
ID AB047367 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 797
ID ABU59825 standard; protein; 660 AA.
DE Novel secreted and transmembrane protein PRO265.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 798
ID ABO25015 standard; protein; 660 AA.
DE Human secreted/transmembrane protein (PRO) #175.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 799
ID ABU64504 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 800
ID ABU72065 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 801
ID ABU67350 standard; protein; 660 AA.
DE Human secreted protein PRO265.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 802	ID ABO1950 standard; protein; 660 AA.
ID DE Novel human secreted and transmembrane protein PRO265.	DE Human PRO polypeptide #175.
PN US2003032062-A1.	PN US2003054517-A1.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 803	RESULT 812
ID ABO14870 standard; protein; 660 AA.	ID ADA61573 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.	DE Homo sapiens.
PN US2003036060-A1.	PN US2003049816-A1.
PD 20-FEB-2003.	PD 13-MAR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 804	RESULT 813
ID ABU67020 standard; protein; 660 AA.	ID ADB19358 standard; protein; 660 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 350.	DE Novel human secreted and transmembrane protein PRO265.
PN US2003032155-A1.	PN US2003068796-A1.
PD 13-FEB-2003.	PD 10-APR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 805	RESULT 814
ID ABU69627 standard; protein; 660 AA.	ID ADB27899 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.	DE Human PRO polypeptide #175.
PN US2003017463-A1.	PN US2003082704-A1.
PD 23-JAN-2003.	PD 01-MAY-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 806	RESULT 815
ID ABU79808 standard; protein; 660 AA.	ID ADA86378 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.	DE Novel human secreted and transmembrane protein PRO265.
PN US2003032057-A1.	PN US2003082711-A1.
PD 13-FEB-2003.	PD 01-MAY-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 807	RESULT 816
ID ABO14809 standard; protein; 660 AA.	ID ADB15942 standard; protein; 660 AA.
DE Human secreted / transmembrane polypeptide PRO265.	DE Human PRO polypeptide #175.
PN US2003027143-A1.	PN US2003087350-A1.
PD 06-FEB-2003.	PD 08-MAY-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 808	RESULT 817
ID ADA45869 standard; protein; 660 AA.	ID ADA47728 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.	DE Human PRO polypeptide #175.
PN US2003022328-A1.	PN US2003073215-A1.
PD 30-JAN-2003.	PD 17-APR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 809	RESULT 818
ID ADA76300 standard; protein; 660 AA.	ID ADA18089 standard; protein; 660 AA.
DE Human PRO polypeptide #175.	DE Human secreted/transmembrane protein, #7.
PN US2003073212-A1.	PN US2003039971-A1.
PD 17-APR-2003.	PD 27-FEB-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 810	RESULT 819
ID ADB29233 standard; protein; 660 AA.	ID ABO32761 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.	DE Human secreted/transmembrane protein PRO265.
PN US2003092002-A1.	PN US2003045693-A1.
PD 15-MAY-2003.	PD 06-MAR-2003.
PA (GETH) GENENTECH INC.	PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;	Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;	Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 811	RESULT 820
ID ADAG7523 standard; protein; 660 AA.	ID ADA67523 standard; protein; 660 AA.

DE Human PRO polypeptide #175.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 821
ID ADB30530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 822
ID ADA85826 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 823
ID ADA97038 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 824
ID ADA79342 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 825
ID ADA87481 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 826
ID ADB16683 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 827
ID ABO34821 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 828
ID ADA16064 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 829
ID ADA91775 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 830
ID ADB14838 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 831
ID ADA47287 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 832
ID ADB18799 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 833
ID ADA94014 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 834
ID ADB19910 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 835
ID ADB13222 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 836
ID ABO43323 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 837
ID ADA74476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 838
ID ADA42209 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054401-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 839
ID ADB24709 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 840
ID ADA82233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 841
ID ADA75196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 842
ID ADA85274 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 843
ID ADA84722 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 844
ID ABO17499 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 845
ID ADB29978 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 846
ID ADA80506 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 847
ID ADA75748 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 848
ID ADA46973 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 849
ID ADB25269 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 850
ID ADA93445 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 851
ID ADB26795 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 852
ID ADB31082 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 853
ID ADA61010 standard; protein; 660 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 854
ID ADB24157 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 855
ID ADA96486 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 856
ID ADA81058 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 885
ID ADB38090 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 886
ID ADB66562 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 887
ID ADB89642 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 888
ID ADB90374 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 889
ID ADB77554 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 890
ID ADB39475 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 891
ID ADB74690 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 892
ID ADB47098 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 893
ID ADB86705 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082697-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 894
ID ADB77310 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 895
ID ADB34467 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 896
ID ADB35571 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 897
ID ADB33915 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 898
ID ADB35019 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 899
ID ADB36123 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 900
ID ADB46518 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 901
ID ADC28336 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 902
ID ADC39536 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059828-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 903
ID ADC40050 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 904
ID ADC18878 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 905
ID ADC34174 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 906
ID ADC29229 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 907
ID ADC28760 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 908
ID ADC40645 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 909
ID ADC19302 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 910
ID ADC33750 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 911
ID ADC12820 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 912
ID ADC50391 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 913
ID ADC71918 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 914
ID ADC59917 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 915
ID ADC52924 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 916
ID ADC57278 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 917
ID ADC60469 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 918
ID ADC50944 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 919
ID ADC65471 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 920
ID ADC54569 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 921
ID ADC53530 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 922
ID ADC59053 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 923
ID ADC5991 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 924
ID ADC58501 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein Seq ID350.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 925
ID ADC12272 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 926
ID ADD03175 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 927
ID ADC90167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 928
ID ADC69586 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 929
ID ADC48475 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;

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RESULT 930
ID AD110004 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 931
ID ADD04579 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 932
ID ADC80535 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 933
ID ADD11042 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 934
ID ADD10335 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
FN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 935
ID ADC47923 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 936
ID ADD04827 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
FN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 937
ID ADC79983 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 938
ID ADD11295 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
FN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 939
ID ADD02551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 940
ID ADD03833 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
FN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 941
ID ADD03409 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
FN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 942
ID ADD41165 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 943
ID ADD52304 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 944
ID ADD53044 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 945
ID ADD53596 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 946
ID ADD37088 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
FN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 947
ID ADD51752 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 948
ID ADD02551 standard; protein; 660 AA.
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DE Human PRO polypeptide #175.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 949
ID ADD01985 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 950
ID ADD54167 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 951
ID ADD92484 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US200319030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 952
ID ADD91380 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US200319055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 953
ID AD803994 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US200319057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 954
ID ADE32291 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 955
ID ADE22223 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 956
ID ADD79447 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 957
ID ADE41983 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199026-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 958
ID ADE17800 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 959
ID ADD91932 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 960
ID ADE33395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 961
ID ADE33947 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 962
ID ADD79999 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 963
ID ADD93036 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 964
ID ADE19456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 965
ID ADE34661 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 966
ID ADE18904 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199026-A1.
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 967
ID ADE43100 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 968
ID ADP95889 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 969
ID ADE22775 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 970
ID ADD78893 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 971
ID ADP32843 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 972
ID ADE42535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 973
ID ADD80551 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 974
ID ADP95979 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 975
ID ADE40863 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 976
ID ADE04662 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 977
ID ADE92791 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 978
ID ADG21500 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 979
ID ADG23141 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 980
ID ADF97476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 981
ID ADG80540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 982
ID ADG79988 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 983
ID ADG63796 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 7; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 984
ID ADH59144 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 994
ID ADNI5929 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 995
ID ADNI16558 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 996
ID ADNI15377 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 997
ID ADNI14825 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 998
ID ADI64051 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 999
ID ADC81087 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
FN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1000
ID ADE79106 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
FN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1001
ID ADD76535 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1002
ID ADD87899 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
FN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;

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RESULT 1003
ID ADE86303 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1004
ID ADE79530 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1005
ID ADE75751 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1006
ID ADE73206 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1007
ID ADE41296 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO polypeptide #23.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1008
ID ADE23327 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1009
ID ADE23879 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1010
ID ADE24522 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1011
ID ADE87347 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1012
ID ADE93343 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1013
ID ADE41210 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1014
ID ADE73741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1015
ID ADE18352 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1016
ID ADE88661 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1017
ID ADE99295 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1018
ID ADE94681 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1019
ID ADE91092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1020
ID ADE95233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 8; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1021
ID ADE93343 standard; protein; 660 AA.
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DE Human PRO polypeptide #175.
PN US2003199060-A1.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1022
ID ADF34924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1023
ID ADE98414 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1024
ID ADE92239 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1025
ID ADE90540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1026
ID ADE91687 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1027
ID ADE98841 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1028
ID ADG40311 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHIER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1029
ID ADF73705 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1030
ID ADG02266 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1031
ID ADG22052 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1032
ID ADG20122 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1033
ID ADF98028 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1034
ID ADG24245 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1035
ID ADF98599 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1036
ID ADG03430 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1037
ID ADF99151 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1038
ID ADG16736 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;

RESULT 1057
ID ADG57435 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1058
ID ADG56883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1059
ID ADG55779 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1060
ID ADG58539 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1061
ID ADG70905 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1062
ID ADG92551 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1063
ID ADG57987 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1064
ID ADG53571 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1065
ID ADG71457 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1066
ID ADG61443 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

ID ADG81644 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1067
ID ADH30606 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1068
ID ADG63645 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1069
ID ADH11973 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1070
ID ADG52395 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1071
ID ADG54123 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1072
ID ADG81092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1073
ID ADG56331 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1074
ID ADH12597 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1075
ID ADG61443 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.

PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1076
ID ADH28530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1077
ID ADG54675 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1078
ID ADG59715 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1079
ID ADH20340 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1080
ID ADH43479 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1081
ID ADH07195 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1082
ID ADH59740 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003215504-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1083
ID ADH06768 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.

PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1084
ID ADI81139 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1085
ID ADI18510 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1086
ID ADI65230 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1087
ID ADI37493 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1088
ID ADG09882 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1089
ID ADH97297 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1090
ID ADI15353 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1091
ID ADG09230 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1092

ID AD114685 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1093
ID ADH60400 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1094
ID AD118280 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1095
ID ADJ99457 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1096
ID ADL08650 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1097
ID ADM24995 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1098
ID ADJ63561 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1099
ID ADM29741 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1100
ID ADJ77456 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038336-A1.

PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1101
ID ADK82824 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1102
ID ADJ65578 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1103
ID ADM27714 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1104
ID ADM42438 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1105
ID ADO06063 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1106
ID ADM28300 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1107
ID ADR10915 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.3e-12;
RESULT 1108
ID ADR17824 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.

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PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A. J.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1109
ID AD195782 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1110
ID AD196334 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1111
ID AD165657 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1112
ID ADS74463 standard; protein; 660 AA.
DE Human secreted/transmembrane protein #7.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1113
ID ADS32286 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2004203125-A1.
PD 14-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1114
ID ADT03270 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2004214269-A1.
PD 28-OCT-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1115
ID ADT03500 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1116
ID ADU06386 standard; protein; 660 AA.
DE Novel bronchial cancer-associated human protein SeqID610.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match
Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
Pred. No. 9.3e-12;
RESULT 1117
ID AB203321 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO265 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
Pred. No. 9.3e-12;
RESULT 1118
ID AEA37738 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 10.2%; Score 320; DB 9; Length 660;
Pred. No. 9.3e-12;
RESULT 1119
ID AEB14067 standard; protein; 660 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match
10.2%; Score 320; DB 9; Length 660;
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Best Local Similarity 22.4%; Pred. No. 9.3e-12;
 RESULT 1120
 ID ADT77808 standard; protein; 452 AA.
 DE Chimeric Nogo receptor polypeptide.
 PN WO2004090103-A2.
 PD 21-OCT-2004.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 10.2%; Score 318.5; DB 8; Length 452;
 Best Local Similarity 27.3%; Pred. No. 7.5e-12;
 RESULT 1121
 ID ADT77802 standard; protein; 452 AA.
 DE Chimeric Nogo receptor polypeptide.
 PN WO2004090103-A2.
 PD 21-OCT-2004.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 10.2%; Score 318.5; DB 8; Length 452;
 Best Local Similarity 27.8%; Pred. No. 7.5e-12;
 RESULT 1122
 ID AAE13006 standard; protein; 713 AA.
 DE Human leucine-rich repeat (LRR) family member protein.
 PN WO200175105-A2.
 PD 11-OCT-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 10.1%; Score 317.5; DB 4; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.5e-11;
 RESULT 1123
 ID AAU91335 standard; protein; 713 AA.
 DE Human novel secreted protein LP223(a).
 PN WO200214358-A2.
 PD 21-FEB-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.1%; Score 316.5; DB 5; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.7e-11;
 RESULT 1124
 ID ASG97991 standard; protein; 713 AA.
 DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.
 PN WO200274959-A2.
 PD 26-SEP-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 10.1%; Score 316.5; DB 5; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.7e-11;
 RESULT 1125
 ID ABU52381 standard; protein; 713 AA.
 DE Human GPCR related protein NOV31a.
 PN WO200279398-A2.
 PD 10-OCT-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 10.1%; Score 316.5; DB 6; Length 713;
 Best Local Similarity 23.1%; Pred. No. 1.7e-11;
 RESULT 1126
 ID ADT77796 standard; protein; 474 AA.
 DE Chimeric Nogo receptor polypeptide.
 PN WO2004090103-A2.
 PD 21-OCT-2004.
 PA (UYRP) UNIV ROCHESTER.
 Query Match 10.0%; Score 314.5; DB 8; Length 474;
 Best Local Similarity 27.8%; Pred. No. 1.4e-11;
 RESULT 1127
 ID AAU91341 standard; protein; 656 AA.
 DE Human novel secreted protein LP223(b).
 PN WO200214358-A2.
 PD 21-FEB-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.0%; Score 313.5; DB 5; Length 656;
 Best Local Similarity 23.6%; Pred. No. 2.4e-11;
 RESULT 1128
 ID ADL24097 standard; protein; 713 AA.
 DE Human NOVX polypeptide #71.
 PN US2004002120-A1.
 PD 01-JAN-2004.
 PA (KEKU) KEKUDA R. T.
 PA (TCHE/) TCHERNEV V. T.
 PA (LIUX/) LIU X.

PA (SPYT/) SPYTEK K A.
 PA (PATT/) PATTURAJAN M.
 PA (BURG/) BURGESS C E.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (GORM/) GORMAN L.
 PA (MALY/) MALYANKAR U M.
 PA (BOLD/) BOLDOG F L.
 PA (GUOX/) GUO X.
 PA (SHEN/) SHENOY S G.
 PA (PADI/) PADIGARU M.
 PA (TAUP/) TAUFIER R J.
 PA (MILL/) MILLER C E.
 PA (CASM/) CASMAN S J.
 PA (PENA/) PENNA C E A.
 PA (GANG/) GANGOLLI E A.
 PA (GUSE/) GUSEV V Y.
 PA (SMIT/) SMITHSON G.
 PA (ZERH/) ZERHUSEN B D.
 PA (GERL/) GERLACH V.
 PA (POCH/) POCHART P F.
 PA (FERN/) FERNANDES E R.
 PA (SHIM/) SHIMKETS R A.
 PA (RAST/) RASTELLI L.
 PA (SPAD/) SPADERNA S K.
 PA (LARO/) LAROCHELLE W J.
 PA (ZHON/) ZHONG M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (VOSS/) VOSS E Z.
 PA (HERR/) HERRMANN J L.
 Query Match 10.0%; Score 313.5; DB 8; Length 713;
 Best Local Similarity 23.1%; Pred. No. 2.6e-11;
 RESULT 1129
 ID AAE09437 standard; protein; 592 AA.
 DE Human sbgrango79a protein.
 PN WO200160850-A1.
 PD 23-AUG-2001.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 Query Match 10.0%; Score 312; DB 4; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1130
 ID AAE25351 standard; protein; 592 AA.
 DE Human LP polypeptide, LP243.
 PN WO200248361-A2.
 PD 20-JUN-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.0%; Score 312; DB 5; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1131
 ID AAU91329 standard; protein; 592 AA.
 DE Human novel secreted protein LP243(b).
 PN WO200214358-A2.
 PD 21-FEB-2002.
 PA (ELIL) LILLY & CO ELI.
 Query Match 10.0%; Score 312; DB 5; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1132
 ID ABP60996 standard; protein; 592 AA.
 DE Novel human protein. SEQ ID 83.
 PN WO200250105-A1.
 PD 27-JUN-2002.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 Query Match 10.0%; Score 312; DB 5; Length 592;
 Best Local Similarity 25.9%; Pred. No. 2.6e-11;
 RESULT 1133
 ID AAU79167 standard; protein; 592 AA.
 DE Human leucine-rich repeat proteins-like protein NOV4.
 PN WO200214368-A2.
 PD 21-FEB-2002.
 PA (CURA-) CURAGEN CORP.

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Query Match      10.0%; Score 312; DB 5; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1134
ID ABG74693 standard; protein; 592 AA.
DE Human CGDD protein 6803363CD1 SEQ ID 19.
PN WO2003014322-A2.
PD 20-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match      10.0%; Score 312; DB 6; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1135
ID ADE03417 standard; protein; 592 AA.
DE Human immunoglobulin superfamily member BGS-2.
PN US2003195163-A1.
PD 16-OCT-2003.
PA (WUSS/) WU S.
PA (KRYL/) KRYSTEK S R.
PA (LEBL/) LEE L.
PA (FEDE/) FEDER J N.
PA (CHEN/) CHENG J D.
Query Match      10.0%; Score 312; DB 7; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1136
ID ADU02709 standard; protein; 592 AA.
DE Novel human polypeptide seqid 1176.
PN WO2004093804-A2.
PD 04-NOV-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match      10.0%; Score 312; DB 8; Length 592;
Best Local Similarity 25.9%; Pred. No. 2.6e-11;
RESULT 1137
ID ABG61770 standard; protein; 608 AA.
DE Novel leucine-rich protein.
PN WO200229058-A2.
PD 11-APR-2002.
PA (CURA-) CURAGEN CORP.
Query Match      10.0%; Score 312; DB 5; Length 608;
Best Local Similarity 25.9%; Pred. No. 2.7e-11;
RESULT 1138
ID ABG97967 standard; protein; 634 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match      9.9%; Score 311; DB 5; Length 634;
Best Local Similarity 24.1%; Pred. No. 3.3e-11;
RESULT 1139
ID ABR55628 standard; protein; 420 AA.
DE Amino acid sequence of rat Nogo-66 receptor homologue NGRH1.
PN WO2003035687-A1.
PD 01-MAY-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS PHARMA GMBH.
Query Match      9.9%; Score 310.5; DB 6; Length 420;
Best Local Similarity 29.8%; Pred. No. 2.2e-11;
RESULT 1140
ID ADT77788 standard; protein; 420 AA.
DE Rat Nogo receptor 2 polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP) UNIV ROCHESTER.
Query Match      9.9%; Score 310.5; DB 8; Length 420;
Best Local Similarity 29.8%; Pred. No. 2.2e-11;
RESULT 1141
ID AAO23115 standard; protein; 674 AA.
DE FLRT1 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match      9.9%; Score 310.5; DB 6; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1142
ID ADH17606 standard; protein; 674 AA.
DE Human NOV19a protein - SEQ ID 296.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match      9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1143
ID ADH17628 standard; protein; 674 AA.
DE Human NOV19l protein - SEQ ID 318.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match      9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1144
ID ADH17630 standard; protein; 674 AA.
DE Human NOV19m protein - SEQ ID 320.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match      9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1145
ID ADH17634 standard; protein; 674 AA.
DE Human NOV19o protein - SEQ ID 324.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match      9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1146
ID ADH17632 standard; protein; 674 AA.
DE Human NOV19n protein - SEQ ID 322.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match      9.9%; Score 310.5; DB 8; Length 674;
Best Local Similarity 21.5%; Pred. No. 3.8e-11;
RESULT 1147
ID ABO27346 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO1865.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match      9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4e-11;
RESULT 1148
ID ABO34232 standard; protein; 585 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match      9.9%; Score 309; DB 6; Length 585;
Best Local Similarity 22.3%; Pred. No. 4e-11;
RESULT 1149
ID AAU29215 standard; protein; 649 AA.
DE Human PRO polypeptide sequence #192.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match      9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1150
ID AAB70533 standard; protein; 649 AA.
DE Human PRO3 protein sequence SEQ ID NO:6.
PN WO200110902-A2.
PD 15-FEB-2001.
PA (CURA-) CURAGEN CORP.
Query Match      9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1151
ID AAB87591 standard; protein; 649 AA.
DE Human PRO1865.
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PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 4; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1152
ID ABG95916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1153
ID ABB84953 standard; protein; 649 AA.
DE Human PRO1865 protein sequence SEQ ID NO:274.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1154
ID ABP70109 standard; protein; 649 AA.
DE Human NOV27a.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1155
ID ABB95559 standard; protein; 649 AA.
DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE//) BAKER K P.
PA (FERE//) FERRARA N.
PA (GERB//) GERBER H.
PA (GERR//) GERRITSEN M E.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (HILL//) HILLAN K J.
PA (MARS//) MARSTERS S A.
PA (PANJ//) PAN J.
PA (PAON//) PAONI N F.
PA (STEP//) STEPHAN J F.
PA (WATA//) WATANABE C K.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Query Match 9.9%; Score 309; DB 5; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1156
ID ABU58591 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1157
ID ABU88139 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1158
ID ABU84454 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1159
ID ABR66328 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1160
ID ABR65718 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1161
ID ABU99658 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1162
ID ABU82897 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1163
ID ABU90018 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1164
ID ABR68267 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1165
ID ABU96320 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1166
ID ABU92751 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1167
ID ASO08828 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1168
ID ASO02880 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1169
ID ABR75034 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1170 22.3%; Pred. No. 4.6e-11;
ID AB94796 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1171 22.3%; Pred. No. 4.6e-11;
ID ABU85769 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1172 22.3%; Pred. No. 4.6e-11;
ID ABU98929 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1173 22.3%; Pred. No. 4.6e-11;
ID ABU98144 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1174 22.3%; Pred. No. 4.6e-11;
ID ABU91850 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1175 22.3%; Pred. No. 4.6e-11;
ID ABU89543 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1176 22.3%; Pred. No. 4.6e-11;
ID ABU86384 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1177 22.3%; Pred. No. 4.6e-11;
ID ABU67597 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1178 22.3%; Pred. No. 4.6e-11;
ID ABU80625 standard; protein; 649 AA.
DE Human PRO protein #192.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1179 22.3%; Pred. No. 4.6e-11;
ID ABU90941 standard; protein; 649 AA.

DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1180 22.3%; Pred. No. 4.6e-11;
ID ABO34000 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003090113-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1181 22.3%; Pred. No. 4.6e-11;
ID ABR99543 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1182 22.3%; Pred. No. 4.6e-11;
ID ABR98933 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1183 22.3%; Pred. No. 4.6e-11;
ID ABO16456 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1184 22.3%; Pred. No. 4.6e-11;
ID ABR92356 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1185 22.3%; Pred. No. 4.6e-11;
ID ABO18997 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1186 22.3%; Pred. No. 4.6e-11;
ID ABR78418 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1187 22.3%; Pred. No. 4.6e-11;
ID ABU72017 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1188 22.3%; Pred. No. 4.6e-11;
ID ABU85154 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1189 22.3%; Pred. No. 4.6e-11;

ID ABO00293 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1190
ID ABO11625 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1191
ID ABO02270 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1192
ID ABU8844 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1193
ID ABUS3539 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1194
ID ABO06340 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1195
ID ABR59376 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1196
ID ABO09438 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1197
ID ABO19302 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036118-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1198
ID ABO11320 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1199
ID ABR66938 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1200
ID ABO16151 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1201
ID ABO13857 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1202
ID ABU71571 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1203
ID ABU65760 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, SEQ ID 384.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1204
ID ABO07608 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1205
ID ABO03795 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1206
ID ABR67243 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1207
ID ABO15846 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1208
ID ABUS6127 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, PRO1865.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1209
ID ABU72352 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2002182638-A1.

PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1210
ID ABU65455 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1211
ID ABU95400 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1212
ID ABU71303 standard; protein; 649 AA.
DE Human PRO1865 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1213
ID ABO07913 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1214
ID ABR70154 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1215
ID ABR69487 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1216
ID ABO01628 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1217
ID ABU81430 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1218
ID ABR60227 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1219
ID ABU91025 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003018168-A1.

PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1220
ID ABR67962 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1221
ID ABR65350 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1222
ID ABR68572 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1223
ID ABR71984 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1224
ID ABU85464 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1225
ID ABU89154 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1226
ID ABU83234 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1227
ID ABU95090 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1228
ID ABU90638 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1229
ID ABU64149 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032111-A1.
PD 13-FEB-2003.

RESULT 1240
ID AB008218 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003040066-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1241
ID ABU92541 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
FN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1242
ID ABU81929 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1243
ID ABU66093 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003036157-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1244
ID ABU81111 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
FN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1245
ID ABR59922 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003032120-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1246
ID ABU94110 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003036155-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1247
ID ABU99963 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003022296-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1248
ID ABR6633 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1249
ID ABR91051 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003040058-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1250
ID ABR53325 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1251
ID ABR94478 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1252
ID ABR79360 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1253
ID ABR86689 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1254
ID ABR86994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1255
ID ABR94783 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1256
ID ABR04710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1257
ID ABR70459 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1258
ID ABR98624 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1259
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1260
ID ABR64740 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1261
ID ABR79665 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1262
ID ABR93056 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1263
ID ABR96015 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1264
ID ABR91235 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1265
ID ABR90328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1266
ID ABR09743 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1267
ID ABR011015 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1268
ID ABR71069 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1269
ID ABR98328 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
FN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
22.3%; Pred. No. 4.6e-11;
RESULT 1270
ID ABR87677 standard; protein; 649 AA.
DE Human PRO polypeptide #192.

PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1271
ID ABU91545 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1272
ID ABU89333 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1273
ID ABU84759 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1274
ID ABR69849 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1275
ID ABUS0226 standard; protein; 649 AA.
DE Human PRO protein #192.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1276
ID ABUS2540 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1277
ID ABU93495 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1278
ID ABO10048 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1279
ID ABO09133 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1280
ID ABUS6504 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003027993-A1.

PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1281
ID ABU10701 standard; protein; 649 AA.
DE Human secreted/transmembrane protein #192.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1282
ID ABU72174 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1283
ID ABUS95710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1284
ID ABUS6919 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1285
ID ABR70764 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1286
ID ABO05115 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1287
ID ABO08523 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1288
ID ABO05730 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1289
ID ABR74119 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1290
ID ABR95711 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1291
ID ABR81008 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1292
ID ABR81313 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1293
ID ABR01009 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1294
ID ABR88611 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1295
ID ABR7432 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1296
ID ABR028916 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1297
ID ABR031661 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1298
ID ABR08078 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1299
ID ABR040558 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.

PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1300
ID ABR035983 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1301
ID ABR04122 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1302
ID ADA78136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1303
ID ABR24917 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1304
ID ABR03185 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1305
ID ABR90441 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1306
ID ABR17355 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1307
ID ABR95101 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1308
ID ABR95406 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1309
ID ADBI1789 standard; protein; 649 AA.
DE Human transmembrane PRO polypeptide (SeqID 132).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1310
ID ABO21644 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1311
ID ABR97908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1312
ID ABR87696 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1313
ID ABM77737 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1314
ID ABM27967 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1315
ID ABM06248 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1316
ID ABM03754 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1317
ID ABM35205 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1318
ID ABM26442 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1319
ID ABO48224 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1320
ID ABR92966 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1321
ID ABO24727 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1322
ID ABM11738 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1323
ID ABM02839 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1324
ID ABM16135 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1325
ID ABO27696 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1326
ID ABM29187 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1327
ID ABM07163 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1328
ID ABM21257 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1329
ID ABM09603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1330
ID ABO41473 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1331
ID ABO36288 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1332
ID ABO43817 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1333
ID ABM76517 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1334
ID ABM76213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1335
ID ABM25832 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;
RESULT 1336
ID ABM26137 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003104543-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 22.3%; Score 309; DB 6; Length 649;

Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1337
ID ABO03490 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003036127-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1338
ID ABO02575 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003040061-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1339
ID ABO44304 standard; protein; 649 AA.
DE Human secreted/transmembrane polypeptide PRO 1865.
FN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1340
ID ABE90746 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003036130-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1341
ID ABR73814 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1342
ID ABO17066 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1343
ID ABR94491 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003044917-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1344
ID ABR75998 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1345
ID ABR71374 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1346
ID AER93271 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003064465-A1.
PD 03-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1347
ID ABR93576 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1348
ID ABR88001 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1349
ID ABO28001 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1350
ID ABO30136 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1351
ID ABO33345 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1352
ID ABO50333 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1353
ID ABO8993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1354
ID ABO36593 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1355
ID ABO35678 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1356
ID ABO39643 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1357
ID ABO10518 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1358
ID ABO12043 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1359
ID ABO52189 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1360
ID ABO52494 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1361
ID ADA19994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1362
ID ABO23812 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1363
ID AOB17377 standard; protein; 649 AA.
DE Human transmembrane PRO polypeptide (SeqID 132).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1364
ID ABR97298 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1365
ID ABR87086 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1366
ID ABM1128 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1367
ID ABM28272 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1368
ID ABO32271 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1369
ID ABM15398 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1370
ID ABM06553 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1371
ID ABM04364 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1372
ID ABM22477 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1373
ID ABM07773 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1374
ID ABO40863 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1375
ID ABM35510 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1376
ID ABM33273 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1377
ID ABO52799 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1378
ID ABO50359 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1379
ID ABU99353 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1380
ID ABO04405 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1381
ID ABO06035 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1382
ID ABM18575 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1383
ID ABR97603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1384
ID ABR80703 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1385
ID ABM01314 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1386
ID ABR88916 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1387
ID ABM13568 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1388
ID ABM20952 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1389
ID ABO42083 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1390
ID ABO42693 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1391
ID ABM10213 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1392
ID ABO38728 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1393
ID ABM32968 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1394
ID ABM22782 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1395
ID ABM74993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1396
ID ADA79928 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1397
ID ABR96383 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1398
ID ABM02534 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1399
ID ABR86476 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1400
ID ABR86781 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1401
ID ABM16745 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1402
ID ABM29797 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064456-A1.
PD 03-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1403
ID ABO29221 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1404
ID ABM24002 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1405
ID ABM23392 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1406
ID ABM22172 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1407
ID ABO37813 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1408
ID ABM28577 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1409
ID ABM28882 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1410
ID ABM66526 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1411
ID ABM75908 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

RESULT 1412
ID ABM34188 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1413
ID ABM34493 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1414
ID ABO20424 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1415
ID ABO21339 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1416
ID ABO22254 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1417
ID ADA20166 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1418
ID ABR96688 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1419
ID ABR85866 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1420
ID ABR99848 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1421
ID ABMU0399 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.


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PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1422
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.
PD 06-MAR-2003.
ID ABM00704 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1423
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068700-A1.
PD 10-APR-2003.
ID ABO29831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1424
ID ABM23697 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1425
ID ABM29492 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1426
ID ABO38423 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1427
ID ABO45723 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1428
ID ABM20647 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1429
ID ADAB1655 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1430
ID ABO16761 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1431
ID ABO18387 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1432
ID ABO22814 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1433
ID ABO23119 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1434
ID ABR92661 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1435
ID ABR81618 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003043744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1436
ID ABM78042 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1437
ID ABR98831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1438
ID ABM26747 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1439
ID ABM13873 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
RESULT 1440
ID ABO28611 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064460-A1.
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PD 03-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1450
ID ABO48529 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1451
ID ABO51579 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1452
ID ABO51884 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1453
ID ABO50664 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1454
ID ABR79788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003040059-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1455
ID ABM17050 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1456
ID ABO18082 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1457
ID ABO21034 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1458
ID ABR96993 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1459
ID ABM12348 standard; protein; 649 AA.

PD 03-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1441
ID ABO30441 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1442
ID ABO7468 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1443
ID ABM04059 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1444
ID ABO37203 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1445
ID ABO41778 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1446
ID ABO35373 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1447
ID ABM25222 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003104340-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1448
ID ABO47614 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1449
ID ABO47919 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1460
ID ABM16440 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1461
ID ABM24307 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1462
ID ABM14788 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1463
ID ABM04669 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1464
ID ABM06858 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1465
ID ABM09298 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1466
ID ABO39338 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1467
ID ABM75603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1468
ID ABM25527 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104541-A1.
PD 05-JUN-2003.

Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1469
ID ABM20037 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1470
ID ABO46943 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1471
ID ABO47248 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1472
ID ADA83453 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1473
ID ABR71679 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1474
ID ABR72289 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1475
ID ABR98628 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1476
ID ABO06998 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1477
ID ABR84951 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1478
ID ABR73509 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054467-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Query Match 22.3%; Pred. No. 4.6e-11;
Best Local Similarity
RESULT 1479
ID ABR76603 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1480
ID ABR73204 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1481
ID ABM18270 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1482
ID ABO20729 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1483
ID ABO25472 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1484
ID ABO25777 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1485
ID ABR94186 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1486
ID ABR80093 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1487
ID ABM11433 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1488

ID ABO33040 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1489
ID ABO30746 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1490
ID ABO31051 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1491
ID ABM27357 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1492
ID ABM30102 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1493
ID ABM05638 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1494
ID ABM15703 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1495
ID ABM08688 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1496
ID ABO42388 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1497
ID ABO38118 standard; protein; 649 AA.

DE Human secreted/transmembrane protein (PRO) #192.
FN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1498
ID ABO46028 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
FN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1499
ID AEM66831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
FN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;
RESULT 1500
ID ADB20496 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
FN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.6e-11;

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OM protein - protein search, using sw model

Run on: January 5, 2006, 13:53:04 ; Search time 167 Seconds
(without alignments)
1496.179 Million cell updates/sec

Perfect score: 3135

Sequence: 1 MCSRVPILLPLLLLLALGPC.....PLMGFPGLQSLPHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA.Main.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
3	3135	100.0	598	3	US-09-944-457-69
70	3135	100.0	598	4	US-10-219-065-104
121	3135	100.0	598	4	US-10-429-667-69
126	3135	100.0	598	4	US-10-677-471-69
127	3135	100.0	598	4	US-10-677-669-69
129	3135	100.0	598	5	US-10-735-014-69
130	3135	100.0	598	5	US-10-854-947-69
131	3135	100.0	598	5	US-10-858-993-69
133	3135	100.0	598	5	US-10-901-400-69
134	3135	100.0	598	5	US-10-858-981-69
136	3135	100.0	598	5	US-10-899-671-69
138	3083.5	98.4	673	3	US-09-782-980-59
164	3083.5	98.4	673	3	US-09-997-428-52
265	3083.5	98.4	673	4	US-10-063-742-16
358	3083.5	98.4	673	4	US-10-806-018-59
359	3083.5	98.4	673	5	US-10-972-317-16
360	3083.5	98.4	673	5	US-10-950-374-52
361	3078.5	98.2	676	4	US-10-029-386-33083
362	2935	93.6	672	4	US-10-050-704-99
363	2935	93.6	672	4	US-10-798-512-99
364	2935	93.6	723	4	US-10-050-704-186
365	2935	93.6	723	4	US-10-798-512-186
366	2490	79.4	673	3	US-09-782-980-68
367	2490	79.4	673	4	US-10-806-018-68
368	2484	79.2	673	4	US-10-487-421-10
369	1178.5	37.6	281	3	US-09-866-050A-648
370	980.5	31.3	307	5	US-10-491-355-18

Search completed: January 5, 2006, 14:04:21

Job time : 193 secs

Sequence 8, Appli
Sequence 188, App
Sequence 192, App
Sequence 190, App
Sequence 8, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 35186, A
Sequence 229, App
Sequence 25, Appli
Sequence 438, App
Sequence 229, App
Sequence 30, Appli
Sequence 58, Appli
Sequence 44, Appli
Sequence 58, Appli
Sequence 100, App
Sequence 100, App
Sequence 2, Appli
Sequence 61, Appli
Sequence 4016, Ap
Sequence 5711, Ap
Sequence 62, Appli
Sequence 62, Appli
Sequence 6, Appli
Sequence 45, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 28, Appli
Sequence 58, Appli
Sequence 115, App
Sequence 45, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 46, Appli
Sequence 45, Appli
Sequence 45, Appli
Sequence 28, Appli
Sequence 46, Appli
Sequence 46, Appli

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OM protein - protein search, using sw model

Run on: January 5, 2006, 13:53:49 ; Search time 14 Seconds
(without alignments)
362.510 Million cell updates/sec

Perfect score: 3135
Sequence: 1 MCSRVPLLLPLLLLLALPGP.....PLMGFPGLQSLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubaa/US08 NEW PUB pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US06 NEW PUB pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US07 NEW PUB pep.*
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- 6: /cgn2_6/ptodata/1/pubaa/US10 NEW PUB pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US11 NEW PUB pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US60 NEW PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3083.5	98.4	673	7	US-11-102-240-16
3	330	10.5	653	7	US-11-135-855-25
4	321	10.2	628	7	US-11-147-047-45
6	312	10.0	592	7	US-11-135-855-24
7	309	9.9	649	7	US-11-102-240-132
11	282.5	9.0	745	7	US-11-135-855-37
12	282	9.0	626	7	US-11-010-748A-1
15	249.5	8.0	479	7	US-11-147-047-44
17	237.5	7.6	344	7	US-11-055-163-6
18	237	7.6	349	7	US-11-147-047-47
19	229	7.3	581	7	US-11-089-872-1
20	227	7.2	310	7	US-11-055-163-7
21	227	7.2	771	7	US-11-147-047-34
22	225.5	7.2	766	7	US-11-147-047-27
25	214.5	6.8	716	7	US-11-147-047-52
26	214	6.8	2828	7	US-11-080-991-54
27	214	6.8	2828	7	US-11-186-284-49
28	212	6.8	310	7	US-11-055-163-9
29	212	6.8	344	7	US-11-055-163-8
31	211	6.7	513	7	US-11-102-240-124
32	209.5	6.7	606	6	US-10-624-932-18
34	205.5	6.6	533	7	US-11-147-047-33
35	201.5	6.4	606	6	US-10-624-932-16
36	200.5	6.4	845	7	US-11-147-047-46
37	199	6.3	256	7	US-11-137-465-34
39	195	6.2	866	7	US-11-147-047-32
1	3083.5	98.4	673	7	US-11-102-240-16
3	330	10.5	653	7	US-11-135-855-25
4	321	10.2	628	7	US-11-147-047-45
6	312	10.0	592	7	US-11-135-855-24
7	309	9.9	649	7	US-11-102-240-132
11	282.5	9.0	745	7	US-11-135-855-37
12	282	9.0	626	7	US-11-010-748A-1
15	249.5	8.0	479	7	US-11-147-047-44
17	237.5	7.6	344	7	US-11-055-163-6
18	237	7.6	349	7	US-11-147-047-47
19	229	7.3	581	7	US-11-089-872-1
20	227	7.2	310	7	US-11-055-163-7
21	227	7.2	771	7	US-11-147-047-34
22	225.5	7.2	766	7	US-11-147-047-27
25	214.5	6.8	716	7	US-11-147-047-52
26	214	6.8	2828	7	US-11-080-991-54
27	214	6.8	2828	7	US-11-186-284-49
28	212	6.8	310	7	US-11-055-163-9
29	212	6.8	344	7	US-11-055-163-8
31	211	6.7	513	7	US-11-102-240-124
32	209.5	6.7	606	6	US-10-624-932-18
34	205.5	6.6	533	7	US-11-147-047-33
35	201.5	6.4	606	6	US-10-624-932-16
36	200.5	6.4	845	7	US-11-147-047-46
37	199	6.3	256	7	US-11-137-465-34
39	195	6.2	866	7	US-11-147-047-32

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126	116	3.7	567	6	US-10-954-468-8	Sequence 8, Appli	203	99	3.2	1532	6	US-10-821-234-914	Sequence 914, App
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132	116	3.7	628	6	US-10-954-468-5	Sequence 5, Appli	209	98	3.1	591	6	US-10-770-726-71	Sequence 71, Appli
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134	115.5	3.7	957	7	US-11-108-172-1065	Sequence 1065, Ap	211	97.5	3.1	236	6	US-10-878-556A-96	Sequence 96, Appli
135	115.5	3.7	1450	6	US-10-055-877-48	Sequence 48, Appli	212	97.5	3.1	426	7	US-11-174-150-44	Sequence 44, Appli
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140	112.5	3.6	1197	6	US-10-055-877-8	Sequence 8, Appli	216	96.5	3.1	585	7	US-11-108-172-1067	Sequence 1067, Ap
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143	111	3.5	1348	6	US-10-995-561-524	Sequence 624, App	219	96	3.1	564	7	US-11-186-284-199	Sequence 199, App
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145	110	3.5	467	7	US-11-000-463-924	Sequence 924, App	221	96	3.1	1873	7	US-11-126-313-29	Sequence 29, Appli
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147	109.5	3.5	187	7	US-11-186-284-195	Sequence 195, App	223	95.5	3.0	522	6	US-10-949-720-425	Sequence 425, App
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154	108	3.4	1236	7	US-11-080-991-68	Sequence 68, Appli	229	95.5	3.0	987	6	US-10-949-720-395	Sequence 395, App
156	107.5	3.4	484	7	US-11-078-735-43	Sequence 43, Appli	230	95.5	3.0	987	6	US-10-821-234-1201	Sequence 1201, Ap
157	107.5	3.4	723	7	US-11-078-735-17	Sequence 17, Appli	231	95.5	3.0	1159	6	US-10-613-744-12	Sequence 12, Appli
158	107	3.4	354	6	US-10-821-234-1618	Sequence 1618, Ap	232	95	3.0	502	7	US-11-122-795-14	Sequence 14, Appli
159	107	3.4	641	7	US-11-094-519A-29	Sequence 29, Appli	233	95	3.0	614	7	US-11-155-492-107	Sequence 107, App
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164	106	3.4	3690	6	US-10-995-561-1016	Sequence 1016, Ap	238	95	3.0	1818	6	US-10-995-561-910	Sequence 910, App
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166	105.5	3.4	457	6	US-10-363-924-2	Sequence 2, Appli	240	95	3.0	2098	6	US-10-055-877-253	Sequence 253, App
167	105.5	3.4	695	6	US-10-966-501-110	Sequence 110, App	241	94.5	3.0	1259	6	US-10-995-561-625	Sequence 625, App
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169	105	3.3	920	6	US-10-821-234-1129	Sequence 1129, Ap	243	94.5	3.0	1315	6	US-10-995-561-630	Sequence 630, App
170	105	3.3	976	6	US-10-966-483-2	Sequence 2, Appli	244	94.5	3.0	1341	6	US-10-995-561-621	Sequence 621, App
171	104.5	3.3	707	7	US-11-186-284-132	Sequence 132, App	245	94.5	3.0	2296	6	US-10-995-561-633	Sequence 633, App
172	104	3.3	306	7	US-11-032-797-7	Sequence 7, Appli	246	94.5	3.0	2355	6	US-10-995-561-623	Sequence 623, App
173	104	3.3	307	7	US-11-000-463-244	Sequence 244, App	247	94.5	3.0	2355	6	US-10-995-561-627	Sequence 627, App
174	104	3.3	432	7	US-11-140-417-4	Sequence 4, Appli	248	94.5	3.0	2384	6	US-10-821-234-1545	Sequence 1545, App
175	104	3.3	438	7	US-11-140-417-2	Sequence 2, Appli	249	94.5	3.0	2386	6	US-10-995-561-626	Sequence 626, App
176	104	3.3	793	6	US-10-995-561-925	Sequence 925, App	250	94	3.0	617	7	US-11-143-980-35	Sequence 35, Appli
177	104	3.3	963	6	US-10-995-561-923	Sequence 923, App	251	94	3.0	838	7	US-11-114-906-40	Sequence 40, Appli
178	104	3.3	1035	6	US-10-966-483-20	Sequence 20, Appli	252	94	3.0	851	7	US-11-114-906-38	Sequence 38, Appli
179	104	3.3	1035	7	US-11-021-441-4	Sequence 4, Appli	253	94	3.0	863	7	US-11-114-906-32	Sequence 32, Appli
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183	102.5	3.3	969	6	US-10-055-877-214	Sequence 214, App	257	94	3.0	976	7	US-11-114-906-28	Sequence 28, Appli
185	102	3.3	3717	6	US-10-821-234-1076	Sequence 1076, Ap	258	94	3.0	982	7	US-11-114-906-26	Sequence 26, Appli
186	101	3.2	360	7	US-11-069-185-7	Sequence 7, Appli	259	94	3.0	2011	7	US-11-080-991-56	Sequence 56, Appli
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191	100	3.2	1897	6	US-10-821-234-1635	Sequence 1635, Ap	264	93.5	3.0	833	7	US-11-076-187-5	Sequence 5, Appli
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277	91.5	2.9	987	7	US-11-052-554A-153	Sequence 153, App	350	86.5	2.8	406	7	US-11-107-028-7	Sequence 7, Appli
278	91.5	2.9	1041	6	US-10-995-561-780	Sequence 780, App	351	86.5	2.8	409	6	US-10-878-556A-55	Sequence 55, Appl
279	91.5	2.9	1041	6	US-10-995-561-782	Sequence 782, App	352	86	2.7	298	7	US-11-080-091-9	Sequence 9, Appli
280	91.5	2.9	1097	6	US-10-995-561-781	Sequence 781, App	353	86	2.7	381	6	US-10-821-234-1342	Sequence 1342, Ap
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291	90	2.9	537	6	US-10-504-364-7	Sequence 7, Appli	364	85.5	2.7	662	7	US-11-090-439-9	Sequence 9, Appli
292	90	2.9	818	7	US-11-037-243-111	Sequence 111, App	365	85.5	2.7	720	7	US-11-102-240-38	Sequence 38, Appl
293	90	2.9	837	7	US-11-127-877-74	Sequence 74, Appl	366	85.5	2.7	837	6	US-10-995-561-698	Sequence 698, App
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296	89.5	2.9	3623	6	US-10-995-561-593	Sequence 593, App	370	85.5	2.7	1165	7	US-11-192-219-2	Sequence 2, Appli
297	89	2.8	484	7	US-11-052-554A-177	Sequence 177, App	371	85.5	2.7	1174	6	US-10-995-561-697	Sequence 697, App
298	89	2.8	1140	6	US-10-055-877-215	Sequence 215, App	372	85.5	2.7	1250	7	US-11-137-465-62	Sequence 62, Appl
299	89	2.8	1892	7	US-11-075-185-6	Sequence 6, Appli	373	85.5	2.7	2764	6	US-10-995-561-691	Sequence 691, App
300	89	2.8	6893	7	US-11-205-109-14	Sequence 14, Appli	374	85.5	2.7	2813	6	US-10-995-561-688	Sequence 688, App
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302	88.5	2.8	494	6	US-10-971-560-7	Sequence 7, Appli	376	85	2.7	479	6	US-10-821-234-871	Sequence 871, App
303	88.5	2.8	663	6	US-10-467-945A-1	Sequence 1, Appli	377	85	2.7	536	6	US-10-641-678-70	Sequence 70, Appl
304	88.5	2.8	993	7	US-11-137-465-36	Sequence 36, Appl	378	85	2.7	595	7	US-11-182-946-9	Sequence 9, Appli
305	88.5	2.8	1210	6	US-10-624-932-26	Sequence 26, Appl	379	85	2.7	614	6	US-10-519-447-2	Sequence 2, Appli
306	88.5	2.8	1263	7	US-11-076-163-3	Sequence 3, Appli	380	85	2.7	614	6	US-10-878-556A-75	Sequence 75, Appl
307	88.5	2.8	1454	7	US-11-109-157A-2	Sequence 2, Appli	381	85	2.7	948	7	US-11-037-243-94	Sequence 94, Appl
308	88.5	2.8	1663	6	US-10-055-877-148	Sequence 148, App	382	84.5	2.7	335	7	US-11-136-619-30	Sequence 30, Appl
309	88.5	2.8	1686	7	US-11-109-157A-1	Sequence 1, Appli	383	84.5	2.7	351	7	US-11-136-619-14	Sequence 14, Appl
310	88.5	2.8	3063	7	US-11-186-284-26	Sequence 26, Appl	384	84.5	2.7	379	7	US-11-136-619-2	Sequence 2, Appli
311	88	2.8	367	6	US-10-888-962-6	Sequence 6, Appli	386	84.5	2.7	379	7	US-11-136-619-22	Sequence 22, Appl
312	87.5	2.8	188	6	US-10-945-853-1	Sequence 1, Appli	387	84.5	2.7	379	7	US-11-136-619-23	Sequence 23, Appl
313	87.5	2.8	269	7	US-11-118-855-17	Sequence 17, Appl	388	84.5	2.7	379	7	US-11-136-619-22	Sequence 22, Appl
314	87.5	2.8	330	7	US-11-124-368A-301	Sequence 301, App	389	84.5	2.7	740	7	US-11-137-465-61	Sequence 61, Appl
315	87.5	2.8	374	7	US-11-136-619-24	Sequence 24, Appl	390	84.5	2.7	1254	6	US-10-528-031-47	Sequence 47, Appl
316	87.5	2.8	434	6	US-10-821-234-1680	Sequence 1680, Ap	391	84.5	2.7	1453	7	US-11-004-057-21	Sequence 21, Appl
317	87.5	2.8	551	6	US-10-821-234-1580	Sequence 1580, Ap	392	84	2.7	302	6	US-10-467-657-4028	Sequence 4028, Ap
318	87.5	2.8	551	6	US-10-504-364-1	Sequence 1, Appli	393	84	2.7	868	6	US-10-821-234-1082	Sequence 1082, Ap
319	87.5	2.8	551	6	US-10-504-364-2	Sequence 2, Appli	394	84	2.7	964	7	US-11-137-465-58	Sequence 58, Appl
320	87.5	2.8	551	6	US-10-504-364-5	Sequence 5, Appli	395	84	2.7	965	7	US-11-147-047-51	Sequence 51, Appl
321	87.5	2.8	749	7	US-11-124-368A-299	Sequence 299, App	396	83.5	2.7	587	7	US-11-000-463-400	Sequence 400, App
322	87.5	2.8	859	7	US-11-124-368A-298	Sequence 298, App	397	83.5	2.7	711	6	US-10-821-234-1017	Sequence 1017, Ap
323	87.5	2.8	877	7	US-11-124-368A-302	Sequence 302, App	398	83.5	2.7	1207	6	US-10-821-234-1109	Sequence 1109, Ap
324	87.5	2.8	963	6	US-10-467-962B-2	Sequence 2, Appli	399	83.5	2.7	1252	7	US-11-039-398-20	Sequence 20, Appl
325	87.5	2.8	1053	7	US-11-052-554A-151	Sequence 151, App	400	83.5	2.7	2647	6	US-10-821-234-1303	Sequence 1303, Ap
326	87.5	2.8	1464	7	US-11-000-463-243	Sequence 243, App	401	83	2.6	176	7	US-11-128-059-72	Sequence 72, Appl
327	87.5	2.8	1464	7	US-11-186-284-28	Sequence 28, Appl	402	83	2.6	232	7	US-11-128-059-66	Sequence 66, Appl
328	87.5	2.8	1467	6	US-10-821-234-1096	Sequence 1096, Ap	403	83	2.6	313	6	US-10-485-517-123	Sequence 123, App
329	87.5	2.8	2339	7	US-11-096-281-11	Sequence 11, Appl	404	83	2.6	313	6	US-10-485-517-293	Sequence 293, App
330	87.5	2.8	3507	7	US-11-075-185-7	Sequence 7, Appli	405	83	2.6	549	7	US-11-096-070-2	Sequence 2, Appli
331	87	2.8	291	6	US-10-995-561-558	Sequence 558, App	406	83	2.6	549	7	US-11-096-070-6	Sequence 6, Appli
332	87	2.8	293	6	US-10-995-561-562	Sequence 562, App	407	83	2.6	721	7	US-11-128-059-88	Sequence 88, Appl
333	87	2.8	318	6	US-10-821-234-1117	Sequence 1117, Ap	408	83	2.6	744	7	US-11-186-284-39	Sequence 39, Appl
334	87	2.8	359	6	US-10-888-962-5	Sequence 5, Appli	409	83	2.6	884	6	US-10-995-561-786	Sequence 786, App
335	87	2.8	438	6	US-10-821-234-1051	Sequence 1051, Ap	410	83	2.6	931	7	US-11-128-059-86	Sequence 86, Appl
336	87	2.8	482	6	US-10-821-234-942	Sequence 942, App	411	83	2.6	1194	7	US-11-000-463-249	Sequence 249, App
337	87	2.8	562	6	US-10-995-561-561	Sequence 561, App	412	83	2.6	1311	6	US-10-509-422-5	Sequence 422, Ap
338	87	2.8	615	6	US-10-995-561-940	Sequence 940, App	413	83	2.6	1327	7	US-11-128-059-92	Sequence 92, Appl
339	87	2.8	662	6	US-10-995-561-943	Sequence 943, App	414	83	2.6	1327	7	US-11-128-059-84	Sequence 84, Appl
340	87	2.8	702	6	US-11-102-240-34	Sequence 34, Appl	415	83	2.6	1416	7	US-11-128-059-4	Sequence 4, Appli
341	87	2.8	754	6	US-10-995-561-942	Sequence 942, App	416	83	2.6	1637	6	US-10-821-234-1204	Sequence 1204, Ap
342	87	2.8	843	7	US-10-995-561-941	Sequence 941, App	417	83	2.6	2086	7	US-11-128-059-82	Sequence 82, Appl
343	87	2.8	1439	7	US-11-129-104-89	Sequence 89, Appl	418	83	2.6	2313	7	US-11-128-059-80	Sequence 80, Appl
344	87	2.8	1439	7	US-11-124-368A-291	Sequence 291, App	419	83	2.6	2358	7	US-11-128-059-74	Sequence 74, Appl
345	87	2.8	2801	7	US-11-124-368A-305	Sequence 305, App	420	83	2.6	2458	7	US-11-128-059-94	Sequence 94, Appl
346	87	2.8	2896	7	US-11-124-368A-306	Sequence 306, App	421	83	2.6	2551	7	US-11-128-059-96	Sequence 96, Appl
							422	82.5	2.6	235	7	US-11-126-126-16	Sequence 16, Appl

423	82.5	2.6	251	6	US-10-528-031-8	Sequence 8, Appli	500	80	2.6	757	7	US-11-052-554A-378	Sequence 378, App
425	82.5	2.6	463	7	US-11-102-240-86	Sequence 86, Appl	501	80	2.6	901	7	US-11-082-389-430	Sequence 430, App
426	82.5	2.6	463	7	US-11-000-463-872	Sequence 872, App	502	80	2.6	1051	7	US-11-205-109-13	Sequence 13, Appl
428	82.5	2.6	510	6	US-10-641-678-43	Sequence 43, Appl	503	80	2.6	1255	6	US-10-770-726-62	Sequence 62, Appl
429	82.5	2.6	511	6	US-10-641-678-42	Sequence 42, Appl	504	80	2.6	1255	7	US-11-113-202-10	Sequence 10, Appl
430	82.5	2.6	526	6	US-10-641-678-46	Sequence 46, Appl	505	80	2.6	4374	7	US-11-128-572-2	Sequence 2, Appli
431	82.5	2.6	615	6	US-10-982-545-14	Sequence 14, Appl	506	79.5	2.5	320	6	US-10-858-730-111	Sequence 111, App
432	82.5	2.6	948	6	US-10-485-517-131	Sequence 131, App	507	79.5	2.5	332	6	US-10-949-720-405	Sequence 405, App
433	82.5	2.6	965	7	US-11-113-424-2	Sequence 2, Appli	508	79.5	2.5	431	6	US-10-949-720-410	Sequence 410, App
434	82.5	2.6	984	6	US-10-995-561-629	Sequence 629, App	509	79.5	2.5	548	7	US-11-137-465-47	Sequence 47, Appl
435	82.5	2.6	1366	6	US-10-821-234-1431	Sequence 1431, Ap	510	79.5	2.5	718	6	US-10-918-857-2	Sequence 2, Appli
436	82.5	2.6	1366	7	US-11-186-284-31	Sequence 31, Appl	511	79.5	2.5	776	6	US-10-925-970-3	Sequence 3, Appli
437	82.5	2.6	1400	6	US-10-821-234-1045	Sequence 1045, Ap	512	79.5	2.5	790	6	US-10-918-857-6	Sequence 6, Appli
438	82.5	2.6	1433	7	US-11-094-519A-40	Sequence 40, Appl	513	79.5	2.5	948	6	US-10-523-477-14	Sequence 14, Appl
439	82.5	2.6	4384	6	US-10-821-234-1120	Sequence 1120, Ap	514	79.5	2.5	2725	7	US-11-113-424-52	Sequence 52, Appl
440	82	2.6	255	6	US-10-467-657-2044	Sequence 2044, Ap	515	79.5	2.5	3674	7	US-11-000-463-454	Sequence 454, App
441	82	2.6	308	6	US-10-967-527A-30	Sequence 30, Appl	516	79	2.5	119	7	US-11-110-424-4	Sequence 4, Appli
442	82	2.6	470	6	US-10-979-821-14	Sequence 14, Appl	517	79	2.5	280	7	US-11-052-554A-318	Sequence 318, App
443	82	2.6	470	7	US-11-114-922-14	Sequence 14, Appl	518	79	2.5	304	7	US-11-080-091-10	Sequence 10, Appl
444	82	2.6	550	6	US-10-504-364-8	Sequence 8, Appli	519	79	2.5	327	6	US-10-454-437-52	Sequence 52, Appl
445	82	2.6	550	6	US-10-504-364-9	Sequence 9, Appli	520	79	2.5	343	7	US-11-080-091-4	Sequence 4, Appli
446	82	2.6	672	7	US-11-000-463-455	Sequence 455, App	521	79	2.5	345	7	US-11-087-177-19	Sequence 19, Appl
447	82	2.6	685	6	US-10-661-966-3	Sequence 3, Appli	522	79	2.5	380	7	US-11-132-864-30	Sequence 30, Appl
448	82	2.6	744	7	US-11-186-284-37	Sequence 37, Appl	523	79	2.5	502	6	US-10-966-483-23	Sequence 23, Appl
449	82	2.6	765	6	US-10-661-966-10	Sequence 10, Appl	524	79	2.5	502	7	US-11-021-441-7	Sequence 7, Appli
450	82	2.6	765	6	US-10-661-966-15	Sequence 15, Appl	525	79	2.5	563	6	US-10-966-483-25	Sequence 25, Appl
451	82	2.6	768	6	US-10-995-561-956	Sequence 956, App	526	79	2.5	563	7	US-11-021-441-9	Sequence 9, Appli
452	82	2.6	783	6	US-10-661-966-2	Sequence 2, Appli	527	79	2.5	574	6	US-10-966-483-31	Sequence 31, Appl
453	82	2.6	830	6	US-10-995-561-957	Sequence 957, App	528	79	2.5	574	7	US-11-021-441-15	Sequence 15, Appl
454	82	2.6	830	6	US-10-995-561-958	Sequence 958, App	529	79	2.5	581	6	US-10-966-483-27	Sequence 27, Appl
455	82	2.6	909	7	US-11-186-284-2	Sequence 2, Appli	530	79	2.5	581	6	US-10-966-483-29	Sequence 29, Appl
456	82	2.6	912	6	US-10-964-313-12	Sequence 12, Appl	531	79	2.5	581	7	US-11-021-441-11	Sequence 11, Appl
457	82	2.6	913	6	US-10-821-234-1040	Sequence 1040, Ap	532	79	2.5	581	7	US-11-021-441-13	Sequence 13, Appl
458	82	2.6	1062	6	US-10-821-234-1079	Sequence 1079, Ap	533	79	2.5	816	7	US-11-090-439-48	Sequence 48, Appl
460	82	2.6	1302	7	US-11-004-057-6	Sequence 6, Appli	534	79	2.5	909	7	US-11-076-187-4	Sequence 4, Appli
461	82	2.6	1463	6	US-10-971-982-3	Sequence 3, Appli	535	79	2.5	925	6	US-10-454-437-50	Sequence 50, Appl
462	82	2.6	1874	6	US-10-821-234-1182	Sequence 1182, Ap	536	79	2.5	1234	6	US-10-985-561-870	Sequence 870, App
464	81.5	2.6	502	6	US-10-689-742-148	Sequence 148, App	537	79	2.5	1366	6	US-10-995-561-868	Sequence 868, App
465	81.5	2.6	574	6	US-10-527-771-14	Sequence 14, Appl	538	79	2.5	1411	6	US-10-995-561-869	Sequence 869, App
466	81.5	2.6	1141	6	US-10-995-561-1009	Sequence 1009, Ap	539	79	2.5	1493	7	US-11-004-057-4	Sequence 4, Appli
467	81.5	2.6	1141	6	US-10-995-561-1010	Sequence 1010, Ap	540	79	2.5	1496	7	US-11-186-284-35	Sequence 35, Appl
468	81	2.6	211	6	US-11-124-368A-187	Sequence 187, App	541	79	2.5	1618	6	US-10-984-645-2	Sequence 2, Appli
469	81	2.6	333	7	US-11-050-440-2	Sequence 2, Appli	542	79	2.5	1841	7	US-11-057-058-63	Sequence 63, Appl
470	81	2.6	825	6	US-10-995-561-679	Sequence 679, App	543	78.5	2.5	236	7	US-11-139-499-10	Sequence 10, Appl
471	81	2.6	852	7	US-11-104-923A-5	Sequence 5, Appli	544	78.5	2.5	287	7	US-11-198-819-6	Sequence 6, Appli
472	81	2.6	1166	6	US-10-821-234-964	Sequence 964, App	545	78.5	2.5	287	7	US-11-198-819-8	Sequence 8, Appli
473	81	2.6	1255	7	US-11-022-562-213	Sequence 213, App	547	78.5	2.5	531	7	US-11-096-070-4	Sequence 4, Appli
474	81	2.6	1466	7	US-11-186-284-33	Sequence 33, Appl	548	78.5	2.5	533	7	US-11-124-368A-335	Sequence 335, App
475	81	2.6	1620	6	US-10-055-877-213	Sequence 213, App	549	78.5	2.5	540	6	US-10-641-678-44	Sequence 44, Appl
476	81	2.6	1664	6	US-10-055-877-212	Sequence 212, App	550	78.5	2.5	997	7	US-11-057-058-33	Sequence 33, Appl
477	81	2.6	2107	6	US-10-995-561-827	Sequence 827, App	551	78.5	2.5	1060	7	US-11-090-739-120	Sequence 120, App
478	81	2.6	2480	6	US-10-995-561-825	Sequence 825, App	552	78.5	2.5	2101	6	US-10-857-780-23	Sequence 23, Appl
479	81	2.6	3116	6	US-10-995-561-826	Sequence 826, App	553	78.5	2.5	3002	6	US-10-821-234-916	Sequence 916, App
480	80.5	2.6	340	6	US-10-999-866-32	Sequence 32, Appl	554	78	2.5	141	6	US-10-467-657-1840	Sequence 1840, Ap
481	80.5	2.6	340	7	US-11-061-821-32	Sequence 32, Appl	555	78	2.5	175	6	US-10-821-234-1074	Sequence 1074, Ap
482	80.5	2.6	523	6	US-10-641-678-45	Sequence 45, Appl	556	78	2.5	408	7	US-11-140-417-6	Sequence 6, Appli
483	80.5	2.6	587	7	US-11-200-109-27	Sequence 27, Appl	557	78	2.5	1178	7	US-11-044-899-29	Sequence 29, Appl
484	80.5	2.6	637	6	US-10-821-234-961	Sequence 961, App	558	78	2.5	1613	7	US-11-108-528-84	Sequence 84, Appl
485	80.5	2.6	1126	7	US-11-110-480-7	Sequence 7, Appli	559	77.5	2.5	175	6	US-10-967-527A-7	Sequence 7, Appli
486	80.5	2.6	1126	7	US-11-110-480-9	Sequence 9, Appli	560	77.5	2.5	298	7	US-11-085-812-4	Sequence 4, Appli
487	80.5	2.6	1126	7	US-11-110-480-16	Sequence 16, Appl	561	77.5	2.5	306	6	US-10-518-341-2	Sequence 2, Appli
488	80.5	2.6	1126	7	US-11-110-480-27	Sequence 27, Appl	562	77.5	2.5	327	7	US-11-165-211-52	Sequence 52, Appl
489	80.5	2.6	1126	7	US-11-110-480-37	Sequence 37, Appl	563	77.5	2.5	327	7	US-11-165-226-62	Sequence 62, Appl
490	80.5	2.6	1126	7	US-11-110-480-47	Sequence 47, Appl	564	77.5	2.5	388	7	US-11-082-389-220	Sequence 220, App
491	80.5	2.6	1126	7	US-11-110-480-59	Sequence 59, Appl	565	77.5	2.5	405	6	US-10-821-234-931	Sequence 931, App
492	80.5	2.6	1126	7	US-11-110-480-82	Sequence 82, Appl	567	77.5	2.5	494	7	US-11-165-697-48	Sequence 48, Appl
493	80.5	2.6	1126	7	US-11-110-480-88	Sequence 88, Appl	568	77.5	2.5	616	6	US-10-982-545-5	Sequence 5, Appli
494	80.5	2.6	1615	7	US-11-110-480-80	Sequence 80, Appl	569	77.5	2.5	696	7	US-11-029-003-8	Sequence 8, Appli
495	80	2.6	156	6	US-10-401-386B-44	Sequence 44, Appl	570	77.5	2.5	1123	7	US-11-037-243-77	Sequence 77, Appl
496	80	2.6	426	7	US-11-055-822-450	Sequence 450, App	571	77.5	2.5	1163	7	US-11-044-899-2	Sequence 2, Appli
497	80	2.6	451	7	US-11-102-240-82	Sequence 82, Appl	572	77.5	2.5	1163	7	US-11-044-899-30	Sequence 30, Appl
498	80	2.6	512	7	US-11-108-172-1093	Sequence 1093, Ap	573	77	2.5	244	7	US-11-052-554A-323	Sequence 323, App
499	80	2.6	589	6	US-10-821-234-1687	Sequence 1687, Ap	574	77	2.5	305	7	US-11-000-463-863	Sequence 863, App

575	77	2.5	345	7	US-11-087-177-21	Sequence 21, Appl	648	74	2.4	114	6	US-10-986-501-116	Sequence 116, App
576	77	2.5	356	6	US-10-821-234-870	Sequence 870, App	649	74	2.4	308	6	US-10-821-234-1332	Sequence 1332, App
577	77	2.5	362	7	US-11-080-091-12	Sequence 12, Appl	650	74	2.4	308	6	US-10-995-561-944	Sequence 944, App
578	77	2.5	414	6	US-10-821-234-1170	Sequence 1170, App	651	74	2.4	364	7	US-11-087-177-31	Sequence 31, Appl
579	77	2.5	422	7	US-11-135-855-33	Sequence 33, Appl	652	74	2.4	364	7	US-11-087-177-33	Sequence 33, Appl
580	77	2.5	494	7	US-11-094-519A-35	Sequence 35, Appl	653	74	2.4	368	7	US-11-000-463-916	Sequence 916, App
581	77	2.5	587	6	US-10-925-970-6	Sequence 6, Appl	654	74	2.4	388	7	US-11-000-463-444	Sequence 444, App
582	77	2.5	736	7	US-11-078-189-11	Sequence 11, Appl	655	74	2.4	401	6	US-10-949-720-419	Sequence 419, App
583	77	2.5	807	6	US-11-102-240-98	Sequence 98, Appl	656	74	2.4	414	7	US-11-115-968-2	Sequence 2, Appl
584	77	2.5	1124	6	US-10-858-730-12	Sequence 12, Appl	657	74	2.4	450	7	US-11-077-386-20	Sequence 20, Appl
585	77	2.5	1215	6	US-10-964-313-6	Sequence 6, Appl	658	74	2.4	504	7	US-11-155-492-73	Sequence 73, Appl
586	77	2.5	1613	7	US-11-108-528-86	Sequence 86, Appl	659	74	2.4	783	7	US-11-186-284-59	Sequence 59, Appl
587	77	2.5	1627	6	US-10-821-234-1283	Sequence 1283, App	660	74	2.4	1431	7	US-11-128-059-2	Sequence 2, Appl
588	77	2.5	2333	7	US-11-096-281-13	Sequence 13, Appl	661	73.5	2.3	115	7	US-11-000-463-252	Sequence 252, App
589	77	2.5	5405	7	US-11-108-172-1116	Sequence 1116, App	662	73.5	2.3	276	6	US-10-467-657-4172	Sequence 4172, App
590	76.5	2.4	188	6	US-10-945-853-2	Sequence 2, Appl	663	73.5	2.3	276	6	US-10-467-657-7078	Sequence 7078, App
591	76.5	2.4	201	7	US-11-094-519A-45	Sequence 45, Appl	664	73.5	2.3	372	6	US-10-650-326B-13	Sequence 13, Appl
592	76.5	2.4	431	6	US-10-995-561-807	Sequence 807, App	665	73.5	2.3	407	6	US-10-698-618-1	Sequence 1, Appl
593	76.5	2.4	431	6	US-10-995-561-808	Sequence 808, App	666	73.5	2.3	470	6	US-10-793-626-2496	Sequence 2496, App
594	76.5	2.4	431	7	US-11-186-284-161	Sequence 161, App	667	73.5	2.3	544	7	US-11-165-226-126	Sequence 126, App
595	76.5	2.4	500	6	US-10-821-234-1458	Sequence 1458, App	668	73.5	2.3	572	6	US-10-821-234-1290	Sequence 1290, App
596	76.5	2.4	500	7	US-11-090-915-2	Sequence 2, Appl	669	73.5	2.3	715	6	US-10-793-626-570	Sequence 570, App
597	76.5	2.4	509	7	US-11-124-327-2	Sequence 2, Appl	670	73.5	2.3	726	7	US-11-124-368A-247	Sequence 247, App
598	76.5	2.4	618	6	US-10-858-730-74	Sequence 74, Appl	671	73.5	2.3	910	6	US-10-793-626-3108	Sequence 3108, App
599	76.5	2.4	736	7	US-11-075-185-9	Sequence 9, Appl	672	73.5	2.3	1128	7	US-11-037-243-97	Sequence 97, Appl
600	600	2.4	790	6	US-10-995-561-955	Sequence 955, App	673	73.5	2.3	1365	6	US-10-995-561-867	Sequence 867, App
601	76.5	2.4	1084	6	US-10-964-313-2	Sequence 2, Appl	674	73.5	2.3	1404	6	US-10-995-561-526	Sequence 526, App
602	76.5	2.4	1562	7	US-11-052-554A-211	Sequence 211, App	675	73	2.3	178	6	US-10-821-234-1495	Sequence 1495, App
603	76	2.4	244	6	US-10-477-507A-4	Sequence 4, Appl	676	73	2.3	232	7	US-11-173-564-2	Sequence 2, Appl
604	76	2.4	330	6	US-11-055-822-524	Sequence 524, App	677	73	2.3	246	6	US-10-467-657-2424	Sequence 2424, App
605	76	2.4	359	7	US-11-087-177-25	Sequence 25, Appl	678	73	2.3	274	7	US-11-015-546A-12	Sequence 12, Appl
606	76	2.4	365	7	US-11-087-177-27	Sequence 27, Appl	679	73	2.3	305	7	US-11-000-463-391	Sequence 391, App
607	76	2.4	456	6	US-10-477-507A-2	Sequence 2, Appl	680	73	2.3	359	7	US-11-087-177-29	Sequence 29, Appl
608	76	2.4	463	7	US-11-069-642-107	Sequence 107, App	681	73	2.3	371	7	US-11-137-671-16	Sequence 16, Appl
609	76	2.4	482	6	US-10-632-150-14	Sequence 14, Appl	682	73	2.3	442	6	US-10-821-234-1594	Sequence 1594, App
610	76	2.4	482	7	US-11-073-457-14	Sequence 14, Appl	683	73	2.3	497	6	US-10-999-866-34	Sequence 34, Appl
611	76	2.4	482	7	US-11-073-460-14	Sequence 14, Appl	684	73	2.3	497	6	US-11-061-821-34	Sequence 34, Appl
612	76	2.4	524	7	US-11-124-368A-286	Sequence 286, App	685	73	2.3	498	6	US-10-467-657-7810	Sequence 7810, App
613	76	2.4	526	7	US-11-124-368A-310	Sequence 310, App	686	73	2.3	533	7	US-11-128-059-58	Sequence 58, Appl
614	76	2.4	556	7	US-11-124-368A-287	Sequence 287, App	687	73	2.3	612	7	US-11-186-284-136	Sequence 136, App
615	76	2.4	608	6	US-10-055-877-121	Sequence 121, App	688	73	2.3	620	7	US-11-186-284-134	Sequence 134, App
616	76	2.4	608	6	US-11-110-082-40	Sequence 40, Appl	689	73	2.3	622	7	US-11-021-441-35	Sequence 35, Appl
617	76	2.4	759	6	US-10-858-730-75	Sequence 75, Appl	690	73	2.3	654	6	US-10-528-031-1	Sequence 1, Appl
618	76	2.4	853	6	US-10-821-234-1110	Sequence 1110, App	691	73	2.3	1416	7	US-11-128-059-60	Sequence 60, Appl
619	76	2.4	907	7	US-11-124-368A-288	Sequence 288, App	692	73	2.3	1494	7	US-11-128-059-78	Sequence 78, Appl
620	76	2.4	1010	7	US-11-052-554A-89	Sequence 89, Appl	693	73	2.3	1510	7	US-11-055-822-72	Sequence 72, Appl
621	76	2.4	1463	7	US-11-080-991-22	Sequence 22, Appl	694	72.5	2.3	140	7	US-11-118-855-11	Sequence 11, Appl
622	75.5	2.4	219	6	US-10-689-742-106	Sequence 106, App	695	72.5	2.3	203	6	US-10-467-657-1560	Sequence 1560, App
623	75.5	2.4	310	6	US-10-994-820A-10	Sequence 10, App	696	72.5	2.3	331	7	US-11-143-980-57	Sequence 57, Appl
624	75.5	2.4	330	7	US-11-085-812-2	Sequence 2, Appl	697	72.5	2.3	334	6	US-10-995-561-822	Sequence 822, App
625	75.5	2.4	516	7	US-11-052-554A-335	Sequence 335, App	698	72.5	2.3	362	7	US-11-052-554A-77	Sequence 77, Appl
626	75.5	2.4	693	6	US-10-995-561-632	Sequence 632, App	699	72.5	2.3	367	6	US-10-821-234-1058	Sequence 1058, App
627	75.5	2.4	810	6	US-10-984-468-37	Sequence 37, Appl	701	72.5	2.3	446	7	US-11-055-822-96	Sequence 96, Appl
628	75.5	2.4	834	7	US-11-052-554A-212	Sequence 212, App	702	72.5	2.3	481	6	US-10-467-657-3916	Sequence 3916, App
629	75	2.4	273	6	US-10-995-561-917	Sequence 917, App	703	72.5	2.3	534	7	US-11-055-822-268	Sequence 268, App
630	75	2.4	360	7	US-11-129-143-113	Sequence 113, App	704	72.5	2.3	541	7	US-11-118-855-26	Sequence 26, Appl
631	75	2.4	393	7	US-11-052-554A-254	Sequence 254, App	705	72.5	2.3	553	7	US-11-055-822-266	Sequence 266, App
632	75	2.4	399	7	US-11-077-386-18	Sequence 18, Appl	706	72.5	2.3	553	7	US-11-110-082-25	Sequence 25, Appl
633	75	2.4	475	6	US-10-509-464-8	Sequence 8, Appl	707	72.5	2.3	618	6	US-10-821-234-1016	Sequence 1016, App
634	75	2.4	588	7	US-11-037-243-100	Sequence 100, App	708	72.5	2.3	686	6	US-10-821-234-1027	Sequence 1027, App
635	75	2.4	585	7	US-11-205-109-26	Sequence 26, App	709	72.5	2.3	773	6	US-10-995-561-852	Sequence 852, App
636	75	2.4	901	6	US-10-793-626-342	Sequence 342, App	710	72.5	2.3	858	6	US-10-995-561-854	Sequence 854, App
637	74.5	2.4	245	6	US-10-467-657-1570	Sequence 1570, App	711	72.5	2.3	943	7	US-11-113-202-8	Sequence 8, Appl
638	74.5	2.4	267	6	US-10-508-263-102	Sequence 102, App	712	72.5	2.3	1142	7	US-11-044-051-73	Sequence 73, Appl
639	74.5	2.4	358	7	US-11-055-822-572	Sequence 572, App	713	72.5	2.3	1178	6	US-10-995-561-851	Sequence 851, App
640	74.5	2.4	358	7	US-11-055-822-836	Sequence 836, App	714	72.5	2.3	1210	7	US-11-113-202-6	Sequence 6, Appl
641	74.5	2.4	427	7	US-11-182-946-5	Sequence 5, Appl	715	72.5	2.3	1210	6	US-11-145-566-1	Sequence 1, Appl
642	74.5	2.4	427	7	US-11-185-878-4	Sequence 4, Appl	716	72.5	2.3	1798	6	US-10-995-561-1033	Sequence 1033, App
643	74.5	2.4	573	6	US-10-525-710-36	Sequence 36, Appl	717	72.5	2.3	1798	6	US-10-995-561-1034	Sequence 1034, App
644	74.5	2.4	777	6	US-10-821-234-1658	Sequence 1658, App	718	72.5	2.3	3157	7	US-11-052-554A-142	Sequence 142, App
645	74.5	2.4	917	6	US-11-144-987-26	Sequence 26, Appl	719	72	2.3	359	6	US-10-055-877-265	Sequence 265, App
646	74.5	2.4	1127	6	US-10-858-730-13	Sequence 13, Appl	720	72	2.3	359	7	US-11-080-091-1	Sequence 1, Appl
647	74.5	2.4	1302	7	US-11-090-439-42	Sequence 42, Appl	721	72	2.3	359	7	US-11-116-939-15	Sequence 15, Appl

722	72	2.3	359	7	US-11-087-177-23	Sequence 23, Appl	800	70.5	2.2	538	7	US-11-124-368A-255	Sequence 255, App
723	72	2.3	442	7	US-11-124-368A-212	Sequence 212, App	801	70.5	2.2	538	7	US-11-124-368A-256	Sequence 256, App
724	72	2.3	455	6	US-10-467-657-5828	Sequence 5828, Ap	802	70.5	2.2	551	6	US-11-000-463-346	Sequence 346, App
725	72	2.3	480	6	US-10-821-234-1465	Sequence 1465, Ap	803	70.5	2.2	578	6	US-10-858-730-103	Sequence 103, App
726	72	2.3	497	7	US-11-143-980-61	Sequence 61, Appl	804	70.5	2.2	579	6	US-10-821-234-1352	Sequence 1352, Ap
727	72	2.3	559	6	US-10-821-234-1513	Sequence 1513, Ap	805	70.5	2.2	586	6	US-10-623-155-152	Sequence 152, App
728	72	2.3	560	7	US-11-080-991-62	Sequence 62, Appl	806	70.5	2.2	586	6	US-10-623-155-338	Sequence 338, App
729	72	2.3	577	7	US-11-124-368A-213	Sequence 213, App	807	70.5	2.2	625	7	US-11-021-441-37	Sequence 37, Appl
730	72	2.3	770	6	US-10-821-234-1269	Sequence 1269, Ap	808	70.5	2.2	641	6	US-10-623-155-339	Sequence 339, App
732	72	2.3	841	6	US-10-624-932-6	Sequence 6, Appli	809	70.5	2.2	680	6	US-10-623-155-342	Sequence 342, App
733	72	2.3	841	6	US-10-624-932-8	Sequence 8, Appli	810	70.5	2.2	686	7	US-11-099-691-9	Sequence 9, Appli
734	72	2.3	883	6	US-10-770-726-57	Sequence 57, Appl	811	70.5	2.2	695	6	US-10-793-626-2922	Sequence 2922, Ap
735	72	2.3	938	7	US-11-109-157A-18	Sequence 18, Appl	812	70.5	2.2	705	6	US-11-102-240-162	Sequence 162, App
736	72	2.3	1198	6	US-10-451-375-4	Sequence 4, Appli	813	70.5	2.2	733	6	US-10-821-234-1147	Sequence 1147, Ap
737	72	2.3	1221	7	US-11-109-157A-17	Sequence 17, Appl	814	70.5	2.2	774	7	US-11-000-463-459	Sequence 459, App
738	72	2.3	2551	7	US-11-052-554A-368	Sequence 368, App	815	70.5	2.2	917	7	US-11-144-987-24	Sequence 24, Appl
739	71.5	2.3	173	6	US-10-667-295-9	Sequence 9, Appli	816	70.5	2.2	4128	6	US-10-770-726-77	Sequence 77, Appl
740	71.5	2.3	280	6	US-10-821-234-1300	Sequence 1300, Ap	817	70	2.2	193	6	US-10-981-873-2	Sequence 2, Appli
741	71.5	2.3	387	7	US-11-137-465-57	Sequence 57, Appl	818	70	2.2	205	7	US-11-098-662-2	Sequence 2, Appli
742	71.5	2.3	411	7	US-11-186-284-51	Sequence 51, Appl	819	70	2.2	208	6	US-10-821-234-1118	Sequence 1118, Ap
743	71.5	2.3	411	7	US-11-102-501-2	Sequence 2, Appli	820	70	2.2	355	7	US-11-182-946-14	Sequence 14, Appl
744	71.5	2.3	419	7	US-11-113-202-2	Sequence 2, Appli	821	70	2.2	401	6	US-10-821-234-881	Sequence 881, App
745	71.5	2.3	461	6	US-10-989-649-1	Sequence 1, Appli	822	70	2.2	411	7	US-11-061-869-12	Sequence 12, Appl
747	71.5	2.3	517	6	US-10-485-517-310	Sequence 310, App	823	70	2.2	453	7	US-11-185-878-5	Sequence 5, Appli
748	71.5	2.3	532	6	US-10-857-780-18	Sequence 18, Appl	824	70	2.2	455	7	US-11-182-946-3	Sequence 3, Appli
749	71.5	2.3	532	6	US-10-995-561-897	Sequence 897, App	825	70	2.2	516	6	US-10-641-678-39	Sequence 39, Appl
750	71.5	2.3	532	7	US-11-104-812-2	Sequence 2, Appli	826	70	2.2	516	6	US-10-641-678-40	Sequence 40, Appl
751	71.5	2.3	532	7	US-11-105-279-2	Sequence 2, Appli	827	70	2.2	516	6	US-10-641-678-41	Sequence 41, Appl
752	71.5	2.3	532	7	US-11-107-028-22	Sequence 22, Appl	828	70	2.2	549	7	US-11-096-070-8	Sequence 8, Appli
753	71.5	2.3	548	7	US-11-132-142-5	Sequence 5, Appli	829	70	2.2	552	6	US-10-821-234-1022	Sequence 1022, Ap
754	71.5	2.3	570	7	US-11-124-368A-196	Sequence 196, App	830	70	2.2	552	7	US-11-135-855-34	Sequence 34, Appl
755	71.5	2.3	621	6	US-10-821-234-1376	Sequence 1376, App	831	70	2.2	666	7	US-11-096-046-27	Sequence 27, Appl
756	71.5	2.3	628	7	US-10-880-991-108	Sequence 108, App	832	70	2.2	716	6	US-10-467-657-6200	Sequence 6200, Ap
757	71.5	2.3	757	6	US-10-055-877-190	Sequence 190, App	833	70	2.2	744	6	US-10-467-657-1936	Sequence 1936, Ap
758	71.5	2.3	771	6	US-10-821-234-1271	Sequence 1271, App	834	70	2.2	915	7	US-11-144-987-22	Sequence 22, Appl
759	71.5	2.3	1011	7	US-11-057-058-31	Sequence 31, Appl	835	70	2.2	1614	7	US-11-108-528-82	Sequence 82, Appl
760	71.5	2.3	1061	7	US-11-000-463-347	Sequence 347, App	836	69.5	2.2	166	7	US-11-000-463-730	Sequence 730, App
761	71.5	2.3	1857	6	US-10-055-877-252	Sequence 252, App	837	69.5	2.2	250	6	US-10-821-234-987	Sequence 987, App
762	71.5	2.3	1970	6	US-10-821-234-1641	Sequence 1641, Ap	838	69.5	2.2	266	6	US-10-821-234-1629	Sequence 1629, Ap
763	71.5	2.3	2109	6	US-10-055-877-251	Sequence 251, App	839	69.5	2.2	304	7	US-11-126-313-26	Sequence 26, Appl
764	71.5	2.3	7968	7	US-11-143-980-49	Sequence 49, Appl	840	69.5	2.2	304	7	US-11-205-109-3	Sequence 3, Appli
765	71	2.3	331	7	US-11-078-735-33	Sequence 33, Appl	841	69.5	2.2	381	6	US-10-454-437-316	Sequence 316, App
766	71	2.3	332	7	US-11-078-735-51	Sequence 51, Appl	842	69.5	2.2	393	7	US-11-077-712-4	Sequence 4, Appli
767	71	2.3	372	6	US-10-844-035-1	Sequence 1, Appli	843	69.5	2.2	404	6	US-10-793-626-2638	Sequence 2638, Ap
768	71	2.3	384	7	US-11-134-563-2	Sequence 2, Appli	844	69.5	2.2	423	7	US-11-000-463-375	Sequence 375, App
769	71	2.3	385	6	US-10-995-561-945	Sequence 945, App	845	69.5	2.2	445	6	US-10-982-545-8	Sequence 8, Appli
770	71	2.3	385	6	US-10-995-561-949	Sequence 949, App	846	69.5	2.2	457	6	US-10-982-545-13	Sequence 13, Appl
771	71	2.3	397	6	US-10-821-234-1020	Sequence 1020, Ap	847	69.5	2.2	457	6	US-10-509-464-7	Sequence 7, Appli
772	71	2.3	435	7	US-11-077-386-19	Sequence 19, Appl	848	69.5	2.2	461	6	US-10-504-364-3	Sequence 3, Appli
773	71	2.3	520	6	US-10-467-657-1992	Sequence 1992, Ap	849	69.5	2.2	558	6	US-10-504-364-4	Sequence 4, Appli
774	71	2.3	538	7	US-11-124-368A-311	Sequence 311, App	850	69.5	2.2	558	6	US-11-205-109-38	Sequence 38, Appl
775	71	2.3	538	7	US-11-124-368A-312	Sequence 312, App	851	69.5	2.2	560	7	US-11-063-343-28	Sequence 28, Appl
776	71	2.3	538	7	US-11-124-368A-313	Sequence 313, App	852	69.5	2.2	596	7	US-11-198-819-22	Sequence 22, Appl
777	71	2.3	856	6	US-10-467-657-8534	Sequence 8534, Ap	853	69.5	2.2	651	7	US-10-510-947-6	Sequence 6, Appli
778	71	2.3	1150	6	US-10-821-234-1083	Sequence 1083, Ap	854	69.5	2.2	654	6	US-10-510-947-6	Sequence 6, Appli
779	71	2.3	2084	6	US-10-055-877-73	Sequence 73, Appl	855	69.5	2.2	667	7	US-11-096-046-28	Sequence 28, Appl
780	71	2.3	2326	7	US-11-126-313-37	Sequence 37, Appl	856	69.5	2.2	667	7	US-11-096-046-30	Sequence 30, Appl
781	71	2.3	2399	7	US-11-052-554A-92	Sequence 92, Appl	857	69.5	2.2	668	7	US-11-111-239-13	Sequence 13, Appl
782	71	2.3	2505	7	US-11-126-313-33	Sequence 33, Appl	858	69.5	2.2	674	6	US-10-055-877-319	Sequence 319, App
783	71	2.3	2769	7	US-11-113-424-14	Sequence 14, Appl	859	69.5	2.2	732	7	US-11-124-368A-248	Sequence 248, App
784	71	2.3	3433	6	US-10-714-781A-67	Sequence 67, Appl	860	69.5	2.2	735	6	US-10-467-657-6990	Sequence 6990, Ap
785	70.5	2.2	205	7	US-11-134-795-27	Sequence 27, Appl	861	69.5	2.2	856	6	US-10-510-947-8	Sequence 8, Appli
786	70.5	2.2	300	7	US-11-154-257-2	Sequence 2, Appli	862	69.5	2.2	856	7	US-11-042-988-13	Sequence 13, Appl
788	70.5	2.2	344	6	US-10-454-437-148	Sequence 148, App	863	69.5	2.2	1138	7	US-11-012-762-28	Sequence 28, Appl
789	70.5	2.2	376	6	US-10-467-657-6138	Sequence 6138, Ap	864	69	2.2	125	6	US-10-821-234-1277	Sequence 1277, Ap
790	70.5	2.2	419	6	US-10-821-234-1556	Sequence 1556, Ap	865	69	2.2	311	6	US-10-980-388-111	Sequence 111, App
791	70.5	2.2	425	6	US-10-995-561-616	Sequence 616, App	866	69	2.2	316	7	US-10-980-388-113	Sequence 113, App
794	70.5	2.2	481	7	US-11-116-939-14	Sequence 14, Appl	867	69	2.2	330	6	US-11-075-185-21	Sequence 21, Appl
795	70.5	2.2	487	7	US-11-124-368A-198	Sequence 198, App	868	69	2.2	530	6	US-10-980-388-62	Sequence 62, Appl
796	70.5	2.2	498	7	US-11-124-368A-254	Sequence 254, App	869	69	2.2	828	6	US-10-995-561-983	Sequence 983, App
797	70.5	2.2	504	7	US-11-186-541-3	Sequence 3, Appli	870	69	2.2	918	6	US-10-995-561-981	Sequence 981, App
798	70.5	2.2	517	6	US-10-954-468-16	Sequence 16, Appl	871	69	2.2	977	7	US-11-093-274-39	Sequence 39, Appl
799	70.5	2.2	538	7	US-11-124-368A-252	Sequence 252, App	872	69	2.2	1019	6	US-10-995-561-982	Sequence 982, App

874	69	2.2	2312	7	US-11-126-313-34	Sequence 34, Appl	949	67.5	2.2	404	7	US-11-052-554A-322	Sequence 322, App
875	69	2.2	3056	7	US-11-109-156-20	Sequence 20, Appl	950	67.5	2.2	447	6	US-10-467-657-5834	Sequence 5834, Ap
876	68.5	2.2	114	7	US-11-124-368A-317	Sequence 317, App	951	67.5	2.2	463	7	US-11-128-900-1	Sequence 1, Appli
877	68.5	2.2	114	7	US-11-124-368A-319	Sequence 319, App	952	67.5	2.2	463	7	US-11-128-900-63	Sequence 63, Appl
878	68.5	2.2	282	7	US-11-080-991-34	Sequence 34, Appl	953	67.5	2.2	475	7	US-11-174-150-45	Sequence 45, Appl
880	68.5	2.2	320	7	US-11-119-098-71	Sequence 71, Appl	954	67.5	2.2	669	6	US-10-878-556A-87	Sequence 87, Appl
881	68.5	2.2	334	6	US-10-858-730-114	Sequence 114, App	955	67.5	2.2	836	6	US-10-821-234-1559	Sequence 1559, Ap
882	68.5	2.2	373	7	US-11-082-389-258	Sequence 258, App	956	67.5	2.2	1015	6	US-10-467-657-180	Sequence 180, App
883	68.5	2.2	374	7	US-11-000-463-453	Sequence 453, App	957	67.5	2.2	1015	6	US-10-467-657-3764	Sequence 3764, Ap
884	68.5	2.2	375	6	US-10-995-561-946	Sequence 946, App	958	67.5	2.2	1058	6	US-10-821-234-1473	Sequence 1473, Ap
885	68.5	2.2	397	7	US-11-058-735-78	Sequence 78, Appl	959	67.5	2.2	1058	6	US-10-878-556A-63	Sequence 63, Appl
886	68.5	2.2	402	6	US-10-650-326B-21	Sequence 21, Appl	960	67.5	2.2	1436	7	US-11-052-554A-140	Sequence 140, App
887	68.5	2.2	402	7	US-11-051-568-29	Sequence 29, Appl	961	67.5	2.2	1596	7	US-11-060-005-4	Sequence 4, Appli
888	68.5	2.2	447	6	US-10-467-657-364	Sequence 364, App	962	67.5	2.2	3011	6	US-10-985-205-3	Sequence 3, Appli
889	68.5	2.2	460	7	US-11-076-163-5	Sequence 5, Appli	963	67	2.1	158	6	US-10-995-561-1031	Sequence 1031, Ap
890	68.5	2.2	522	7	US-11-022-562-216	Sequence 216, App	964	67	2.1	158	6	US-10-995-561-1032	Sequence 1032, Ap
891	68.5	2.2	532	7	US-11-143-980-41	Sequence 41, Appl	965	67	2.1	207	7	US-11-075-400-6	Sequence 6, Appli
892	68.5	2.2	565	6	US-10-055-877-228	Sequence 228, App	966	67	2.1	243	7	US-11-147-047-40	Sequence 40, Appl
893	68.5	2.2	585	6	US-11-127-877-63	Sequence 63, Appl	967	67	2.1	274	7	US-11-143-980-58	Sequence 58, Appl
894	68.5	2.2	606	6	US-10-763-712A-9	Sequence 9, Appli	968	67	2.1	351	7	US-11-118-809-6	Sequence 6, Appli
895	68.5	2.2	606	6	US-10-763-712A-97	Sequence 97, Appli	969	67	2.1	373	6	US-10-821-234-1263	Sequence 1263, Ap
896	68.5	2.2	671	7	US-11-029-003-6	Sequence 6, Appli	970	67	2.1	411	6	US-10-989-649-3	Sequence 3, Appli
897	68.5	2.2	772	6	US-10-858-730-77	Sequence 77, Appl	971	67	2.1	411	7	US-11-061-869-16	Sequence 16, Appl
898	68.5	2.2	898	6	US-10-624-332-2	Sequence 2, Appli	972	67	2.1	420	7	US-11-124-368A-194	Sequence 194, App
899	68	2.2	107	7	US-11-123-896-269	Sequence 269, App	973	67	2.1	437	7	US-11-061-869-13	Sequence 13, Appl
900	68	2.2	135	7	US-11-100-338-49	Sequence 49, App	974	67	2.1	437	7	US-11-197-721-11	Sequence 11, Appl
901	68	2.2	137	6	US-10-986-501-349	Sequence 349, App	975	67	2.1	449	7	US-11-196-459-2	Sequence 2, Appli
902	68	2.2	250	6	US-10-821-234-1297	Sequence 1297, Ap	976	67	2.1	473	6	US-10-467-657-298	Sequence 298, App
903	68	2.2	309	7	US-11-124-368A-197	Sequence 197, App	977	67	2.1	473	6	US-10-467-657-6328	Sequence 6328, Ap
904	68	2.2	339	7	US-11-010-874-6	Sequence 6, Appli	978	67	2.1	487	7	US-11-113-424-57	Sequence 57, Appl
905	68	2.2	363	7	US-11-055-822-616	Sequence 616, App	979	67	2.1	513	6	US-10-821-234-1112	Sequence 1112, Ap
906	68	2.2	377	7	US-11-102-621-113	Sequence 113, App	980	67	2.1	567	6	US-10-995-561-764	Sequence 764, App
907	68	2.2	377	7	US-11-102-621-115	Sequence 115, App	981	67	2.1	658	6	US-10-821-234-921	Sequence 921, App
908	68	2.2	416	7	US-11-016-706-38	Sequence 38, Appl	982	67	2.1	672	7	US-11-004-057-2	Sequence 2, Appli
909	68	2.2	425	6	US-10-821-234-990	Sequence 990, App	983	67	2.1	734	6	US-10-852-893-2	Sequence 2, Appli
910	68	2.2	429	7	US-11-093-274-37	Sequence 37, Appl	984	67	2.1	734	7	US-11-137-465-65	Sequence 65, Appl
911	68	2.2	437	6	US-10-632-150-54	Sequence 54, Appl	985	67	2.1	791	7	US-11-056-621-4	Sequence 4, Appli
912	68	2.2	437	7	US-11-073-457-54	Sequence 54, Appl	986	67	2.1	810	6	US-10-995-561-761	Sequence 761, App
913	68	2.2	437	7	US-11-073-460-54	Sequence 54, Appl	987	67	2.1	810	6	US-10-220-824-2	Sequence 2, Appli
914	68	2.2	438	6	US-10-995-561-589	Sequence 589, App	988	67	2.1	1886	6	US-10-515-868-8	Sequence 8, Appli
915	68	2.2	463	7	US-11-128-900-4	Sequence 4, Appli	989	67	2.1	2105	7	US-11-052-554A-173	Sequence 173, App
916	68	2.2	463	7	US-11-128-900-68	Sequence 68, Appl	990	66.5	2.1	108	6	US-10-925-366A-316	Sequence 316, App
917	68	2.2	464	7	US-11-128-900-2	Sequence 2, Appli	991	66.5	2.1	176	7	US-11-055-822-1084	Sequence 1084, Ap
918	68	2.2	464	7	US-11-128-900-66	Sequence 66, Appl	992	66.5	2.1	181	6	US-10-821-234-867	Sequence 867, App
919	68	2.2	477	6	US-10-995-561-587	Sequence 587, App	993	66.5	2.1	205	7	US-11-098-662-6	Sequence 6, Appli
920	68	2.2	477	6	US-10-995-561-588	Sequence 588, App	994	66.5	2.1	301	7	US-11-147-047-37	Sequence 37, Appl
921	68	2.2	478	6	US-10-793-626-1348	Sequence 1348, Ap	995	66.5	2.1	304	7	US-11-087-177-4	Sequence 4, Appli
922	68	2.2	492	6	US-10-148-606-1	Sequence 1, Appli	996	66.5	2.1	406	7	US-11-000-463-377	Sequence 377, App
923	68	2.2	543	6	US-10-432-483-26	Sequence 26, Appl	997	66.5	2.1	423	6	US-11-000-463-849	Sequence 849, App
924	68	2.2	561	7	US-11-124-368A-195	Sequence 195, App	998	66.5	2.1	437	6	US-10-793-626-3160	Sequence 3160, Ap
925	68	2.2	740	7	US-11-110-837-2	Sequence 2, Appli	999	66.5	2.1	437	6	US-10-967-648A-2	Sequence 2, Appli
926	68	2.2	740	7	US-11-110-837-4	Sequence 4, Appli	1000	66.5	2.1	444	6	US-10-467-657-3076	Sequence 3076, Ap
927	68	2.2	759	6	US-10-467-657-2722	Sequence 2722, Ap	1001	66.5	2.1	463	7	US-11-128-900-64	Sequence 64, Appl
928	68	2.2	798	6	US-10-770-726-64	Sequence 64, Appl	1002	66.5	2.1	513	6	US-10-641-678-66	Sequence 66, Appl
929	68	2.2	798	7	US-11-110-082-39	Sequence 39, Appl	1003	66.5	2.1	538	7	US-11-174-398-16	Sequence 16, Appl
930	68	2.2	830	6	US-10-055-877-32	Sequence 32, Appl	1004	66.5	2.1	695	7	US-11-096-046-26	Sequence 26, Appl
931	68	2.2	1113	7	US-11-067-811-4	Sequence 4, Appli	1005	66.5	2.1	750	7	US-11-124-368A-244	Sequence 244, App
932	68	2.2	1172	7	US-11-186-284-203	Sequence 203, App	1006	66.5	2.1	750	7	US-11-124-368A-249	Sequence 249, App
933	68	2.2	1189	6	US-10-821-234-1209	Sequence 1209, Ap	1007	66.5	2.1	758	7	US-11-052-554A-262	Sequence 262, App
934	68	2.2	1417	7	US-11-052-554A-8	Sequence 8, Appli	1008	66.5	2.1	760	6	US-10-858-730-76	Sequence 76, Appl
935	67.5	2.2	210	7	US-11-052-554A-328	Sequence 328, App	1009	66.5	2.1	944	7	US-11-057-058-68	Sequence 68, Appl
936	67.5	2.2	218	7	US-11-143-980-64	Sequence 64, Appl	1010	66.5	2.1	1116	6	US-10-485-517-238	Sequence 238, App
937	67.5	2.2	248	7	US-11-052-554A-56	Sequence 56, Appl	1011	66.5	2.1	1117	6	US-10-485-517-206	Sequence 206, App
938	67.5	2.2	281	7	US-11-034-569-12	Sequence 12, Appl	1012	66.5	2.1	1126	7	US-11-075-185-3	Sequence 3, Appli
939	67.5	2.2	290	6	US-10-821-234-862	Sequence 862, App	1013	66.5	2.1	1232	7	US-11-039-398-18	Sequence 18, Appl
940	67.5	2.2	294	6	US-10-055-877-128	Sequence 128, App	1014	66.5	2.1	1342	6	US-10-770-726-63	Sequence 63, Appl
941	67.5	2.2	304	7	US-11-134-563-4	Sequence 4, Appli	1015	66.5	2.1	1342	7	US-11-113-202-12	Sequence 12, Appl
942	67.5	2.2	307	6	US-10-055-877-263	Sequence 263, App	1016	66.5	2.1	1342	7	US-11-113-202-14	Sequence 14, Appl
943	67.5	2.2	362	7	US-11-052-554A-204	Sequence 204, App	1017	66	2.1	29	6	US-10-945-853-8	Sequence 8, Appli
944	67.5	2.2	364	7	US-11-091-334-2	Sequence 2, Appli	1018	66	2.1	236	7	US-11-022-289-12	Sequence 12, Appl
945	67.5	2.2	377	6	US-10-999-866-37	Sequence 37, Appl	1020	66	2.1	280	7	US-11-071-062-3	Sequence 3, Appli
946	67.5	2.2	377	7	US-11-061-821-37	Sequence 37, Appl	1021	66	2.1	292	6	US-10-972-587-34	Sequence 34, Appl
947	67.5	2.2	399	6	US-10-821-234-1163	Sequence 1163, Ap	1022	66	2.1	232	7	US-11-071-062-5	Sequence 5, Appli

1023	66	2.1	297	6	US-10-821-234-977	Sequence 977, App	1097	65	2.1	504	6	US-10-641-678-36	Sequence 36, Appl
1024	66	2.1	310	7	US-11-055-822-140	Sequence 140, App	1098	65	2.1	529	7	US-11-186-541-1	Sequence 1, Appl
1025	66	2.1	379	7	US-11-132-864-2	Sequence 2, Appl	1099	65	2.1	537	7	US-11-037-243-104	Sequence 104, App
1026	66	2.1	379	7	US-11-132-864-6	Sequence 6, Appl	1100	65	2.1	555	7	US-11-124-368A-300	Sequence 300, App
1027	66	2.1	384	7	US-11-075-351-32	Sequence 32, Appl	1101	65	2.1	565	7	US-11-127-877-68	Sequence 68, Appl
1028	66	2.1	429	7	US-11-071-062-9	Sequence 9, Appl	1102	65	2.1	579	6	US-10-623-155-176	Sequence 176, App
1029	66	2.1	431	7	US-11-058-735-79	Sequence 79, Appl	1103	65	2.1	579	6	US-10-623-155-348	Sequence 348, App
1030	66	2.1	448	6	US-10-967-527A-16	Sequence 16, Appl	1104	65	2.1	579	6	US-10-623-155-446	Sequence 446, App
1031	66	2.1	449	7	US-11-071-082-1	Sequence 1, Appl	1105	65	2.1	579	6	US-10-623-155-449	Sequence 449, App
1032	66	2.1	451	7	US-11-128-900-70	Sequence 70, Appl	1106	65	2.1	579	6	US-10-623-155-480	Sequence 480, App
1033	66	2.1	459	7	US-11-186-284-12	Sequence 12, Appl	1107	65	2.1	579	6	US-10-623-155-484	Sequence 484, App
1034	66	2.1	466	7	US-11-110-082-33	Sequence 33, Appl	1108	65	2.1	580	6	US-10-995-561-987	Sequence 987, App
1035	66	2.1	495	6	US-10-770-726-81	Sequence 81, Appl	1109	65	2.1	586	6	US-10-623-155-427	Sequence 427, App
1036	66	2.1	496	7	US-11-110-082-31	Sequence 31, Appl	1110	65	2.1	589	6	US-10-623-155-486	Sequence 486, App
1037	66	2.1	497	6	US-10-641-678-28	Sequence 28, Appl	1111	65	2.1	657	7	US-11-110-082-37	Sequence 37, Appl
1038	66	2.1	537	7	US-11-186-284-12	Sequence 12, Appl	1112	65	2.1	712	6	US-10-995-561-984	Sequence 984, App
1039	66	2.1	574	6	US-10-821-234-1624	Sequence 1624, Ap	1113	65	2.1	756	6	US-10-055-877-189	Sequence 189, App
1040	66	2.1	599	7	US-11-109-157A-3	Sequence 3, Appl	1114	65	2.1	769	6	US-10-995-561-985	Sequence 985, App
1041	66	2.1	660	7	US-11-186-284-125	Sequence 125, App	1115	65	2.1	769	6	US-10-995-561-986	Sequence 986, App
1042	66	2.1	708	6	US-10-821-234-917	Sequence 917, App	1116	65	2.1	769	7	US-11-107-028-5	Sequence 5, Appl
1043	66	2.1	756	6	US-10-055-877-34	Sequence 34, Appl	1117	65	2.1	865	7	US-11-109-156-4	Sequence 4, Appl
1044	66	2.1	756	6	US-10-055-877-187	Sequence 187, App	1118	65	2.1	985	7	US-11-113-424-61	Sequence 61, Appl
1045	66	2.1	756	6	US-10-055-877-188	Sequence 188, App	1119	65	2.1	1124	7	US-11-195-197-9	Sequence 9, Appl
1046	66	2.1	892	7	US-11-082-389-396	Sequence 396, App	1120	65	2.1	1704	7	US-11-075-046-40	Sequence 40, Appl
1047	66	2.1	1235	7	US-11-039-398-16	Sequence 16, Appl	1121	65	2.1	2515	7	US-11-113-424-53	Sequence 53, Appl
1048	66	2.1	1307	6	US-10-995-561-711	Sequence 711, App	1122	65	2.1	2523	7	US-11-052-554A-143	Sequence 143, App
1049	66	2.1	2314	7	US-11-097-728-2	Sequence 2, Appl	1123	64.5	2.1	185	6	US-10-821-234-1498	Sequence 1498, Ap
1050	66	2.1	2353	7	US-11-097-728-6	Sequence 6, Appl	1124	64.5	2.1	185	6	US-10-529-118-2	Sequence 2, Appl
1051	66	2.1	3144	7	US-11-055-035-1	Sequence 1, Appl	1125	64.5	2.1	232	6	US-10-821-234-1023	Sequence 1023, Ap
1052	65.5	2.1	127	7	US-11-186-284-171	Sequence 171, App	1126	64.5	2.1	248	7	US-11-080-628-23	Sequence 23, Appl
1053	65.5	2.1	180	6	US-10-821-234-978	Sequence 978, App	1127	64.5	2.1	261	6	US-10-821-234-1582	Sequence 1582, Ap
1054	65.5	2.1	190	7	US-11-055-822-958	Sequence 958, App	1128	64.5	2.1	261	6	US-10-878-556A-51	Sequence 51, Appl
1055	65.5	2.1	190	6	US-10-793-626-2370	Sequence 2370, Ap	1129	64.5	2.1	291	6	US-10-972-587-32	Sequence 32, Appl
1056	65.5	2.1	309	6	US-10-793-626-418	Sequence 418, App	1130	64.5	2.1	326	7	US-11-102-621-11	Sequence 11, Appl
1057	65.5	2.1	373	6	US-11-075-351-42	Sequence 42, Appl	1131	64.5	2.1	355	6	US-10-995-793-78	Sequence 78, Appl
1058	65.5	2.1	374	7	US-11-055-822-402	Sequence 402, App	1132	64.5	2.1	355	7	US-11-124-368A-200	Sequence 200, App
1059	65.5	2.1	442	7	US-11-055-822-402	Sequence 402, App	1133	64.5	2.1	355	7	US-11-124-368A-204	Sequence 204, App
1060	65.5	2.1	453	6	US-10-878-556A-141	Sequence 141, App	1134	64.5	2.1	367	7	US-11-000-463-899	Sequence 899, App
1061	65.5	2.1	465	7	US-11-082-389-284	Sequence 284, App	1135	64.5	2.1	389	7	US-11-108-528-68	Sequence 68, Appl
1062	65.5	2.1	467	7	US-11-124-368A-323	Sequence 323, App	1136	64.5	2.1	416	6	US-10-467-657-5060	Sequence 5060, Ap
1063	65.5	2.1	473	7	US-11-124-368A-325	Sequence 325, App	1137	64.5	2.1	452	7	US-11-074-176-274	Sequence 274, App
1064	65.5	2.1	488	6	US-10-821-234-1654	Sequence 1654, Ap	1138	64.5	2.1	458	7	US-11-183-914-11	Sequence 11, Appl
1065	65.5	2.1	488	7	US-11-186-284-121	Sequence 121, App	1139	64.5	2.1	470	6	US-10-878-556A-101	Sequence 101, App
1066	65.5	2.1	499	6	US-10-770-726-74	Sequence 74, Appl	1140	64.5	2.1	470	7	US-11-144-248-45	Sequence 45, Appl
1067	65.5	2.1	501	7	US-11-124-368A-324	Sequence 324, App	1141	64.5	2.1	470	7	US-11-144-222-45	Sequence 45, Appl
1068	65.5	2.1	517	6	US-10-641-678-47	Sequence 47, Appl	1142	64.5	2.1	497	6	US-10-641-678-30	Sequence 30, Appl
1069	65.5	2.1	547	7	US-11-156-003-16	Sequence 16, Appl	1143	64.5	2.1	531	7	US-11-008-727-18	Sequence 18, Appl
1070	65.5	2.1	639	6	US-10-821-234-907	Sequence 907, App	1144	64.5	2.1	557	7	US-11-191-374-4	Sequence 4, Appl
1071	65.5	2.1	639	7	US-11-113-837-21	Sequence 21, Appl	1145	64.5	2.1	557	7	US-11-191-375-4	Sequence 4, Appl
1072	65.5	2.1	667	7	US-10-793-626-2416	Sequence 2416, Ap	1146	64.5	2.1	557	7	US-11-191-588-4	Sequence 4, Appl
1073	65.5	2.1	667	7	US-11-096-046-35	Sequence 25, Appl	1147	64.5	2.1	557	7	US-11-110-082-24	Sequence 24, Appl
1074	65.5	2.1	700	6	US-10-995-561-922	Sequence 922, App	1148	64.5	2.1	654	7	US-11-087-227-14	Sequence 14, Appl
1075	65.5	2.1	700	6	US-10-995-561-924	Sequence 924, App	1149	64.5	2.1	719	7	US-11-191-374-12	Sequence 12, Appl
1076	65.5	2.1	730	6	US-10-821-234-1019	Sequence 1019, Ap	1150	64.5	2.1	881	7	US-11-191-375-12	Sequence 12, Appl
1077	65.5	2.1	742	6	US-10-658-986-2	Sequence 2, Appl	1151	64.5	2.1	881	7	US-11-191-588-10	Sequence 10, Appl
1078	65.5	2.1	755	7	US-11-067-121-6	Sequence 6, Appl	1152	64.5	2.1	881	7	US-11-113-424-60	Sequence 60, Appl
1079	65.5	2.1	777	6	US-10-658-986-4	Sequence 4, Appl	1153	64.5	2.1	984	7	US-11-108-172-1095	Sequence 10, Appl
1080	65.5	2.1	844	6	US-10-763-712A-48	Sequence 48, Appl	1154	64.5	2.1	1170	6	US-10-858-730-71	Sequence 71, Appl
1081	65.5	2.1	904	6	US-10-967-648A-14	Sequence 14, Appl	1155	64.5	2.1	1210	7	US-11-191-375-10	Sequence 10, Appl
1082	65.5	2.1	1091	7	US-11-000-463-348	Sequence 348, App	1156	64.5	2.1	1210	7	US-11-191-375-10	Sequence 10, Appl
1083	65.5	2.1	1213	7	US-11-039-398-14	Sequence 14, Appl	1157	64.5	2.1	1210	7	US-11-191-588-10	Sequence 10, Appl
1084	65.5	2.1	1308	7	US-11-113-202-16	Sequence 16, Appl	1158	64.5	2.1	1548	7	US-11-108-172-1095	Sequence 1095, Ap
1085	65.5	2.1	2096	6	US-10-995-561-606	Sequence 606, App	1159	64.5	2.1	1751	7	US-11-103-957-45	Sequence 45, Appl
1086	65.5	2.1	2351	6	US-10-995-561-608	Sequence 608, App	1160	64.5	2.1	2910	7	US-11-087-100-2	Sequence 2, Appl
1087	65	2.1	176	7	US-10-052-554A-197	Sequence 197, App	1161	64.5	2.1	2910	7	US-11-087-084-2	Sequence 2, Appl
1088	65	2.1	215	6	US-10-374-954-7	Sequence 7, Appl	1162	64	2.0	100	6	US-10-821-234-1135	Sequence 1135, Ap
1089	65	2.1	277	7	US-11-132-285-3	Sequence 3, Appl	1163	64	2.0	146	7	US-11-061-821-42	Sequence 42, Appl
1090	65	2.1	277	7	US-11-182-946-12	Sequence 12, Appl	1164	64	2.0	157	7	US-11-075-046-48	Sequence 48, Appl
1091	65	2.1	294	6	US-10-467-657-2754	Sequence 2754, Ap	1165	64	2.0	164	6	US-11-061-821-42	Sequence 42, Appl
1092	65	2.1	325	6	US-10-454-437-406	Sequence 466, App	1166	64	2.0	190	7	US-11-063-343-30	Sequence 30, Appl
1093	65	2.1	425	7	US-11-061-869-10	Sequence 10, Appl	1167	64	2.0	201	6	US-10-821-234-1006	Sequence 1006, Ap
1094	65	2.1	425	7	US-11-197-721-8	Sequence 8, Appl	1168	64	2.0	211	6	US-10-858-730-102	Sequence 102, App
1095	65	2.1	438	7	US-11-186-541-2	Sequence 2, Appl	1169	64	2.0	218	6	US-10-667-295-151	Sequence 151, App
1096	65	2.1	497	6	US-10-641-678-22	Sequence 22, Appl	1170	64	2.0				

1171	64	2.0	218	7	US-11-188-281-6	Sequence 6, Appli	1246	63.5	2.0	670	6	US-10-995-561-528	Sequence 528, App
1172	64	2.0	218	7	US-11-188-281-17	Sequence 17, Appl	1247	63.5	2.0	714	7	US-11-121-419-17	Sequence 17, Appl
1173	64	2.0	234	6	US-10-821-234-1515	Sequence 1515, Ap	1248	63.5	2.0	774	6	US-10-055-877-191	Sequence 191, App
1174	64	2.0	234	6	US-11-188-281-3	Sequence 3, Appli	1249	63.5	2.0	816	7	US-11-057-058-10	Sequence 10, Appl
1175	64	2.0	285	6	US-10-821-234-983	Sequence 983, App	1250	63.5	2.0	854	7	US-11-022-562-219	Sequence 219, App
1176	64	2.0	291	6	US-10-467-657-1418	Sequence 418, Ap	1251	63.5	2.0	886	6	US-10-873-528-126	Sequence 126, App
1177	64	2.0	309	7	US-11-205-109-24	Sequence 24, Appl	1252	63.5	2.0	923	7	US-11-052-554A-147	Sequence 147, App
1178	64	2.0	337	6	US-10-821-234-1004	Sequence 1004, Ap	1253	63.5	2.0	950	6	US-10-981-267-24	Sequence 24, Appl
1179	64	2.0	373	6	US-10-995-561-948	Sequence 948, App	1254	63.5	2.0	952	6	US-10-821-234-1557	Sequence 1557, Ap
1180	64	2.0	406	6	US-10-821-234-1026	Sequence 1026, Ap	1255	63.5	2.0	952	6	US-11-057-058-54	Sequence 54, Appl
1181	64	2.0	449	7	US-11-196-459-1	Sequence 1, Appli	1256	63.5	2.0	979	6	US-10-636-320-6	Sequence 6, Appli
1182	64	2.0	462	7	US-11-197-721-13	Sequence 13, Appl	1257	63.5	2.0	1107	7	US-11-057-058-41	Sequence 41, Appl
1183	64	2.0	474	7	US-11-055-822-432	Sequence 432, App	1258	63.5	2.0	1162	6	US-10-451-375-3	Sequence 3, Appli
1184	64	2.0	475	7	US-11-061-869-15	Sequence 15, Appl	1259	63.5	2.0	1346	7	US-11-060-005-2	Sequence 2, Appli
1185	64	2.0	478	6	US-10-821-234-915	Sequence 915, App	1260	63.5	2.0	1476	6	US-10-647-956A-4	Sequence 4, Appli
1186	64	2.0	519	7	US-11-099-691-10	Sequence 10, Appl	1261	63.5	2.0	1572	7	US-11-143-380-46	Sequence 46, Appl
1187	64	2.0	547	6	US-10-770-726-87	Sequence 87, Appl	1262	63	2.0	213	7	US-11-120-338-13	Sequence 13, Appl
1188	64	2.0	611	7	US-11-082-389-436	Sequence 436, App	1263	63	2.0	213	7	US-11-107-028-31	Sequence 31, Appl
1189	64	2.0	612	6	US-10-821-234-1101	Sequence 1101, Ap	1264	63	2.0	246	7	US-11-128-440-18	Sequence 18, Appl
1190	64	2.0	672	6	US-10-467-657-5126	Sequence 5126, Ap	1265	63	2.0	248	7	US-11-128-440-19	Sequence 19, Appl
1191	64	2.0	674	7	US-11-167-048-1	Sequence 1, Appli	1266	63	2.0	250	7	US-11-128-440-20	Sequence 20, Appl
1192	64	2.0	675	7	US-11-075-046-52	Sequence 52, Appl	1267	63	2.0	266	6	US-10-467-657-5258	Sequence 5258, Ap
1193	64	2.0	757	7	US-11-067-121-16	Sequence 16, Appl	1268	63	2.0	311	7	US-11-108-172-1061	Sequence 1061, Ap
1194	64	2.0	757	7	US-11-186-284-41	Sequence 41, Appl	1269	63	2.0	333	6	US-10-980-388-91	Sequence 91, Appl
1195	64	2.0	765	6	US-10-821-234-1164	Sequence 1164, Ap	1270	63	2.0	383	6	US-10-467-657-5602	Sequence 5602, Ap
1196	64	2.0	812	7	US-11-010-874-1	Sequence 1, Appli	1271	63	2.0	384	6	US-10-999-866-33	Sequence 33, Appl
1197	64	2.0	826	7	US-11-055-822-214	Sequence 214, App	1272	63	2.0	384	7	US-11-061-821-33	Sequence 33, Appl
1198	64	2.0	835	7	US-11-055-822-712	Sequence 712, App	1273	63	2.0	386	7	US-11-060-029-13	Sequence 13, Appl
1199	64	2.0	833	7	US-11-055-822-212	Sequence 212, App	1274	63	2.0	390	6	US-10-467-657-4288	Sequence 4288, Ap
1200	64	2.0	833	7	US-11-055-822-710	Sequence 710, App	1275	63	2.0	391	7	US-11-055-822-652	Sequence 652, App
1201	64	2.0	858	6	US-10-613-744-6	Sequence 6, Appli	1276	63	2.0	445	6	US-10-467-657-1584	Sequence 1584, Ap
1202	64	2.0	955	7	US-11-052-554A-179	Sequence 179, App	1277	63	2.0	449	6	US-10-763-712A-21	Sequence 21, Appl
1203	64	2.0	995	7	US-11-113-424-62	Sequence 62, Appl	1278	63	2.0	449	6	US-10-763-712A-104	Sequence 104, App
1204	64	2.0	1221	6	US-10-858-730-222	Sequence 222, App	1279	63	2.0	505	7	US-11-063-343-38	Sequence 38, Appl
1205	64	2.0	1554	7	US-11-186-284-93	Sequence 93, Appl	1280	63	2.0	506	6	US-10-467-657-2434	Sequence 2434, Ap
1206	63.5	2.0	108	6	US-10-925-366A-192	Sequence 192, App	1281	63	2.0	521	7	US-11-143-980-32	Sequence 32, Appl
1207	63.5	2.0	127	7	US-11-052-554A-312	Sequence 312, App	1282	63	2.0	589	6	US-10-821-234-1494	Sequence 1494, Ap
1208	63.5	2.0	143	6	US-10-995-951A-30	Sequence 30, Appl	1283	63	2.0	615	7	US-11-198-819-16	Sequence 16, Appl
1209	63.5	2.0	143	6	US-11-067-425A-65	Sequence 65, Appl	1284	63	2.0	615	7	US-11-198-819-18	Sequence 18, Appl
1210	63.5	2.0	188	6	US-10-793-626-3272	Sequence 3272, Ap	1285	63	2.0	628	7	US-11-094-519A-28	Sequence 28, Appl
1211	63.5	2.0	197	6	US-10-467-657-1982	Sequence 1982, Ap	1286	63	2.0	646	6	US-10-491-096-190	Sequence 190, App
1212	63.5	2.0	197	6	US-10-632-150-32	Sequence 32, Appl	1287	63	2.0	708	6	US-10-636-320-2	Sequence 2, Appli
1213	63.5	2.0	197	7	US-11-073-457-32	Sequence 32, Appl	1288	63	2.0	708	7	US-11-196-475-76	Sequence 76, Appl
1214	63.5	2.0	197	7	US-11-073-460-32	Sequence 32, Appl	1289	63	2.0	747	7	US-11-018-018-1	Sequence 1, Appli
1215	63.5	2.0	218	6	US-11-194-246-402	Sequence 402, App	1290	63	2.0	747	7	US-11-047-757-1	Sequence 1, Appli
1216	63.5	2.0	218	6	US-10-821-234-1196	Sequence 1196, Ap	1291	63	2.0	776	6	US-10-821-234-1171	Sequence 1171, Ap
1217	63.5	2.0	234	6	US-10-508-863-100	Sequence 100, App	1292	63	2.0	879	7	US-11-022-562-340	Sequence 340, App
1218	63.5	2.0	271	6	US-10-857-780-19	Sequence 19, Appl	1293	63	2.0	918	6	US-10-995-561-696	Sequence 696, App
1219	63.5	2.0	271	7	US-11-107-028-25	Sequence 25, Appl	1294	63	2.0	937	7	US-11-057-058-55	Sequence 55, Appl
1220	63.5	2.0	286	6	US-10-454-437-78	Sequence 78, Appl	1295	63	2.0	1216	7	US-11-039-398-12	Sequence 12, Appl
1221	63.5	2.0	287	7	US-11-080-991-66	Sequence 66, Appl	1296	63	2.0	1219	7	US-11-039-398-10	Sequence 10, Appl
1222	63.5	2.0	305	6	US-10-055-877-126	Sequence 126, App	1297	62.5	2.0	79	6	US-10-952-535A-21	Sequence 21, Appl
1223	63.5	2.0	305	6	US-10-857-780-19	Sequence 284, App	1298	62.5	2.0	185	6	US-10-967-527A-32	Sequence 32, Appl
1224	63.5	2.0	305	7	US-11-080-091-2	Sequence 2, Appli	1299	62.5	2.0	241	6	US-10-467-657-3300	Sequence 3300, Ap
1225	63.5	2.0	305	7	US-11-087-177-7	Sequence 7, Appli	1300	62.5	2.0	260	7	US-11-055-822-436	Sequence 436, App
1226	63.5	2.0	312	7	US-11-055-822-868	Sequence 868, App	1301	62.5	2.0	275	6	US-10-467-657-2242	Sequence 2242, Ap
1227	63.5	2.0	324	6	US-10-698-618-2	Sequence 2, Appli	1302	62.5	2.0	298	6	US-10-467-657-2850	Sequence 2850, Ap
1228	63.5	2.0	325	7	US-11-102-240-64	Sequence 64, Appl	1303	62.5	2.0	298	6	US-10-467-657-6750	Sequence 6750, Ap
1229	63.5	2.0	331	6	US-10-432-483-25	Sequence 25, Appl	1304	62.5	2.0	343	6	US-10-497-135-11	Sequence 11, Appl
1230	63.5	2.0	345	6	US-11-210-316-14	Sequence 14, Appl	1305	62.5	2.0	355	6	US-10-967-527A-22	Sequence 22, Appl
1231	63.5	2.0	359	6	US-10-467-657-1676	Sequence 1676, Ap	1306	62.5	2.0	376	7	US-11-075-185-15	Sequence 15, Appl
1232	63.5	2.0	371	6	US-10-995-561-572	Sequence 572, App	1307	62.5	2.0	389	7	US-11-108-528-70	Sequence 70, Appl
1233	63.5	2.0	392	6	US-10-793-626-2494	Sequence 2494, Ap	1308	62.5	2.0	447	6	US-10-884-730-379	Sequence 379, App
1234	63.5	2.0	457	6	US-10-821-234-1185	Sequence 1185, Ap	1309	62.5	2.0	454	6	US-10-055-877-204	Sequence 204, App
1235	63.5	2.0	484	6	US-10-873-528-38	Sequence 38, Appl	1310	62.5	2.0	465	6	US-10-967-648A-6	Sequence 6, Appli
1236	63.5	2.0	488	6	US-10-821-234-877	Sequence 877, App	1311	62.5	2.0	474	7	US-11-000-463-284	Sequence 284, App
1237	63.5	2.0	509	7	US-11-008-727-16	Sequence 16, Appl	1312	62.5	2.0	502	6	US-10-454-437-134	Sequence 134, App
1238	63.5	2.0	513	7	US-11-000-463-458	Sequence 458, App	1313	62.5	2.0	506	6	US-10-641-678-69	Sequence 69, App
1239	63.5	2.0	515	7	US-11-093-274-38	Sequence 38, Appl	1314	62.5	2.0	510	6	US-10-641-678-20	Sequence 20, Appl
1240	63.5	2.0	529	6	US-11-122-144-2	Sequence 2, Appli	1315	62.5	2.0	517	7	US-11-074-176-184	Sequence 184, App
1241	63.5	2.0	529	6	US-10-793-626-1376	Sequence 1376, Ap	1316	62.5	2.0	595	6	US-10-510-386-240	Sequence 240, App
1242	63.5	2.0	559	6	US-11-155-492-3	Sequence 3, Appli	1317	62.5	2.0	597	6	US-10-884-730-381	Sequence 381, App
1243	63.5	2.0	616	7	US-11-055-822-522	Sequence 522, App	1318	62.5	2.0	600	6	US-10-606-302-3	Sequence 3, Appli
1244	63.5	2.0	625	7			1319	62.5	2.0				

1321	62.5	2.0	640	7	US-11-094-519A-44	Sequence 44, Appl	1396	61.5	2.0	213	7	US-11-052-554A-291	Sequence 291, Appl
1322	62.5	2.0	648	7	US-11-114-906-12	Sequence 12, Appl	1397	61.5	2.0	251	7	US-11-054-515-68	Sequence 68, Appl
1323	62.5	2.0	654	7	US-11-114-906-10	Sequence 10, Appl	1398	61.5	2.0	260	6	US-10-485-517-354	Sequence 354, App
1324	62.5	2.0	655	7	US-11-079-122-12	Sequence 12, Appl	1399	61.5	2.0	261	6	US-10-485-517-150	Sequence 150, App
1325	62.5	2.0	655	7	US-11-079-122-13	Sequence 13, Appl	1400	61.5	2.0	278	6	US-10-793-822-2344	Sequence 2344, Ap
1326	62.5	2.0	655	7	US-11-079-122-15	Sequence 15, Appl	1401	61.5	2.0	280	6	US-11-055-822-444	Sequence 444, App
1327	62.5	2.0	732	7	US-11-078-189-14	Sequence 14, Appl	1402	61.5	2.0	286	6	US-10-821-234-940	Sequence 940, App
1328	62.5	2.0	747	6	US-10-995-561-840	Sequence 840, App	1403	61.5	2.0	287	7	US-11-174-150-30	Sequence 30, Appl
1330	62.5	2.0	747	6	US-11-124-368A-270	Sequence 270, App	1404	61.5	2.0	288	7	US-11-135-855-30	Sequence 30, Appl
1331	62.5	2.0	753	7	US-11-137-465-51	Sequence 51, Appl	1405	61.5	2.0	305	7	US-11-080-091-13	Sequence 13, Appl
1332	62.5	2.0	772	7	US-11-147-238-2	Sequence 2, Appl	1406	61.5	2.0	305	7	US-11-087-177-11	Sequence 11, Appl
1333	62.5	2.0	772	7	US-11-147-238-5	Sequence 5, Appl	1407	61.5	2.0	305	7	US-11-087-177-13	Sequence 13, Appl
1334	62.5	2.0	773	6	US-10-821-234-1134	Sequence 1134, Ap	1408	61.5	2.0	327	6	US-10-821-234-884	Sequence 884, App
1335	62.5	2.0	778	6	US-10-821-234-1276	Sequence 1276, Ap	1409	61.5	2.0	352	7	US-11-108-528-20	Sequence 20, Appl
1336	62.5	2.0	864	7	US-11-114-906-4	Sequence 4, Appl	1410	61.5	2.0	362	7	US-11-013-247A-7	Sequence 7, Appl
1337	62.5	2.0	870	7	US-11-114-906-2	Sequence 2, Appl	1411	61.5	2.0	364	7	US-11-013-247A-6	Sequence 6, Appl
1338	62.5	2.0	889	7	US-11-114-906-20	Sequence 20, Appl	1412	61.5	2.0	376	7	US-11-116-939-8	Sequence 8, Appl
1339	62.5	2.0	895	7	US-11-114-906-18	Sequence 18, Appl	1414	61.5	2.0	403	7	US-11-205-109-23	Sequence 23, Appl
1340	62.5	2.0	1222	7	US-11-039-398-8	Sequence 8, Appl	1415	61.5	2.0	436	7	US-11-124-368A-236	Sequence 236, App
1341	62.5	2.0	2725	7	US-11-096-051-8	Sequence 8, Appl	1416	61.5	2.0	438	7	US-11-087-121-19	Sequence 19, Appl
1342	62	2.0	172	7	US-11-052-554A-325	Sequence 325, App	1417	61.5	2.0	445	7	US-11-115-564-3	Sequence 3, Appl
1343	62	2.0	176	7	US-11-052-554A-39	Sequence 39, Appl	1418	61.5	2.0	448	7	US-11-013-247A-5	Sequence 5, Appl
1344	62	2.0	200	7	US-11-098-662-18	Sequence 18, Appl	1419	61.5	2.0	471	6	US-10-467-657-6022	Sequence 6022, Ap
1345	62	2.0	205	6	US-10-995-561-1028	Sequence 1028, Ap	1420	61.5	2.0	476	7	US-11-139-499-12	Sequence 12, Appl
1346	62	2.0	205	6	US-10-995-561-1029	Sequence 1029, Ap	1421	61.5	2.0	497	6	US-10-641-678-2	Sequence 2, Appl
1347	62	2.0	213	7	US-11-120-338-16	Sequence 16, Appl	1422	61.5	2.0	497	6	US-10-641-678-6	Sequence 6, Appl
1348	62	2.0	213	7	US-11-107-028-44	Sequence 44, Appl	1423	61.5	2.0	497	6	US-10-641-678-8	Sequence 8, Appl
1349	62	2.0	240	6	US-10-689-742-210	Sequence 210, App	1424	61.5	2.0	497	6	US-10-641-678-10	Sequence 10, Appl
1350	62	2.0	278	7	US-11-113-424-43	Sequence 43, Appl	1425	61.5	2.0	497	6	US-10-641-678-12	Sequence 12, Appl
1352	62	2.0	316	6	US-10-467-657-74	Sequence 74, Appl	1426	61.5	2.0	497	6	US-10-641-678-14	Sequence 14, Appl
1353	62	2.0	316	6	US-10-467-657-74	Sequence 74, Appl	1427	61.5	2.0	497	6	US-10-641-678-16	Sequence 16, Appl
1354	62	2.0	341	6	US-10-821-234-1628	Sequence 3912, Ap	1428	61.5	2.0	497	6	US-10-641-678-18	Sequence 18, Appl
1355	62	2.0	348	6	US-10-467-657-8200	Sequence 8200, Ap	1429	61.5	2.0	497	6	US-10-641-678-24	Sequence 24, Appl
1356	62	2.0	353	6	US-10-055-877-30	Sequence 30, Appl	1430	61.5	2.0	501	7	US-11-013-247A-2	Sequence 2, Appl
1357	62	2.0	357	6	US-10-821-234-1325	Sequence 1325, Ap	1431	61.5	2.0	519	6	US-10-523-477-8	Sequence 8, Appl
1358	62	2.0	363	6	US-10-454-437-94	Sequence 94, Appl	1432	61.5	2.0	529	7	US-11-013-247A-17	Sequence 17, Appl
1359	62	2.0	404	7	US-11-075-351-23	Sequence 23, Appl	1433	61.5	2.0	540	6	US-10-821-234-1395	Sequence 1395, Ap
1360	62	2.0	446	7	US-11-117-667-2	Sequence 2, Appl	1434	61.5	2.0	652	6	US-10-873-528-26	Sequence 26, Appl
1361	62	2.0	447	6	US-10-967-527A-14	Sequence 14, Appl	1435	61.5	2.0	652	7	US-11-079-122-11	Sequence 11, Appl
1362	62	2.0	447	7	US-11-102-621-130	Sequence 130, App	1436	61.5	2.0	711	7	US-11-087-100-18	Sequence 18, Appl
1363	62	2.0	447	7	US-11-102-621-131	Sequence 131, App	1437	61.5	2.0	711	7	US-11-087-084-18	Sequence 18, Appl
1364	62	2.0	447	7	US-11-102-621-132	Sequence 132, App	1438	61.5	2.0	711	7	US-11-087-085-18	Sequence 18, Appl
1365	62	2.0	447	7	US-11-102-621-133	Sequence 133, App	1439	61.5	2.0	714	7	US-11-121-419-2	Sequence 2, Appl
1366	62	2.0	447	7	US-11-102-621-134	Sequence 134, App	1440	61.5	2.0	734	7	US-11-093-274-40	Sequence 40, Appl
1367	62	2.0	450	7	US-11-025-712-12	Sequence 12, Appl	1441	61.5	2.0	736	7	US-11-145-035-22	Sequence 22, Appl
1368	62	2.0	463	6	US-10-793-626-960	Sequence 960, App	1442	61.5	2.0	763	7	US-11-013-247A-35	Sequence 35, Appl
1369	62	2.0	485	6	US-10-204-029-7	Sequence 7, Appl	1443	61.5	2.0	826	6	US-10-873-528-194	Sequence 194, App
1370	62	2.0	487	7	US-11-113-424-56	Sequence 56, Appl	1444	61.5	2.0	860	6	US-11-189-521-2	Sequence 2, Appl
1371	62	2.0	489	6	US-10-858-730-198	Sequence 198, App	1445	61.5	2.0	950	6	US-10-467-657-854	Sequence 854, App
1372	62	2.0	489	7	US-11-035-822-1152	Sequence 1152, Ap	1446	61.5	2.0	956	7	US-11-016-706-40	Sequence 40, Appl
1373	62	2.0	526	7	US-11-035-822-124	Sequence 124, App	1447	61.5	2.0	987	6	US-10-770-726-61	Sequence 61, Appl
1374	62	2.0	572	6	US-10-454-437-68	Sequence 68, Appl	1448	61.5	2.0	1058	7	US-11-069-642-105	Sequence 105, App
1375	62	2.0	584	6	US-10-454-437-66	Sequence 66, Appl	1449	61.5	2.0	1161	7	US-11-075-646-8	Sequence 8, Appl
1376	62	2.0	589	7	US-11-082-389-22	Sequence 22, Appl	1450	61.5	2.0	1207	7	US-11-124-368A-263	Sequence 263, App
1377	62	2.0	603	6	US-10-770-726-75	Sequence 75, Appl	1451	61.5	2.0	1390	7	US-11-053-343-35	Sequence 35, Appl
1378	62	2.0	606	6	US-10-055-877-58	Sequence 58, Appl	1452	61.5	2.0	2015	7	US-11-052-554A-374	Sequence 374, App
1379	62	2.0	650	6	US-10-467-657-1948	Sequence 1948, Ap	1453	61.5	2.0	3353	7	US-11-037-243-64	Sequence 64, App
1380	62	2.0	739	7	US-11-082-389-94	Sequence 94, Appl	1454	61	1.9	91	6	US-10-821-234-1103	Sequence 1103, Ap
1381	62	2.0	744	6	US-10-873-528-184	Sequence 184, App	1455	61	1.9	107	7	US-11-120-338-2	Sequence 2, Appl
1382	62	2.0	875	6	US-10-933-025-12	Sequence 12, Appl	1456	61	1.9	107	7	US-11-107-028-29	Sequence 29, Appl
1383	62	2.0	875	6	US-10-933-025-18	Sequence 18, Appl	1457	61	1.9	193	7	US-11-085-775-4	Sequence 4, Appl
1384	62	2.0	878	7	US-11-103-957-7	Sequence 7, Appl	1458	61	1.9	205	7	US-11-055-822-654	Sequence 654, App
1385	62	2.0	942	6	US-10-770-726-76	Sequence 76, Appl	1460	61	1.9	218	7	US-11-155-845-48	Sequence 48, Appl
1386	62	2.0	959	6	US-10-467-962B-4	Sequence 4, Appl	1461	61	1.9	249	7	US-11-054-515-1321	Sequence 1321, Ap
1387	62	2.0	997	7	US-11-080-991-50	Sequence 50, Appl	1462	61	1.9	251	7	US-11-054-515-2125	Sequence 2125, Ap
1388	62	2.0	1007	6	US-10-467-657-8514	Sequence 8514, Ap	1463	61	1.9	251	7	US-11-054-515-2128	Sequence 2128, Ap
1389	62	2.0	1070	7	US-11-147-047-49	Sequence 49, Appl	1464	61	1.9	257	7	US-11-036-051-12	Sequence 12, Appl
1390	62	2.0	1345	7	US-11-052-554A-282	Sequence 282, App	1465	61	1.9	296	7	US-11-036-051-18	Sequence 18, Appl
1391	62	2.0	1732	6	US-10-055-877-147	Sequence 147, App	1466	61	1.9	303	7	US-11-135-855-31	Sequence 31, Appl
1392	61.5	2.0	94	6	US-10-995-561-603	Sequence 603, App	1467	61	1.9	308	6	US-10-793-626-1732	Sequence 1732, Ap
1393	61.5	2.0	94	6	US-10-995-561-604	Sequence 604, App	1468	61	1.9	308	7	US-11-055-822-822	Sequence 822, App
1394	61.5	2.0	206	6	US-10-467-657-6368	Sequence 6368, Ap	1469	61	1.9	384	7	US-11-075-351-12	Sequence 12, Appl
1395	61.5	2.0	208	7	US-11-114-922-84	Sequence 84, Appl	1473	61	1.9	437	7	US-11-073-626-3	Sequence 3, Appl

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1475	61	1.9	457	6	US-10-467-557-6640	Sequence 6640, Ap
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1477	61	1.9	469	7	US-11-124-368A-321	Sequence 321, App
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1479	61	1.9	470	7	US-11-144-248-49	Sequence 49, Appl
1480	61	1.9	470	7	US-11-144-222-46	Sequence 46, Appl
1481	61	1.9	470	7	US-11-144-222-49	Sequence 49, Appl
1482	61	1.9	473	7	US-11-144-248-50	Sequence 50, Appl
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1484	61	1.9	496	7	US-11-165-697-50	Sequence 50, Appl
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1486	61	1.9	535	6	US-10-935-561-610	Sequence 610, App
1487	61	1.9	559	6	US-10-521-162-4	Sequence 4, Appli
1488	61	1.9	565	7	US-11-080-991-100	Sequence 100, App
1489	61	1.9	598	7	US-11-055-822-820	Sequence 820, App
1490	61	1.9	619	6	US-10-821-234-1150	Sequence 1150, Ap
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1492	61	1.9	720	7	US-11-113-424-28	Sequence 28, Appl
1493	61	1.9	747	7	US-11-113-424-26	Sequence 26, Appl
1494	61	1.9	821	7	US-11-096-051-6	Sequence 6, Appli
1495	61	1.9	861	6	US-10-467-557-1286	Sequence 1286, Ap
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